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OM nucleic - nucleic search, using sw model1

Run on: January 12, 2005, 05:06:55 ; Search time 2053 Seconds
(without alignments)
822.840 Million cell updates/sec

Title: US-10-001-254-5
Perfect score: 294
Sequence: 1 acatcgtgcgcgtccca.....tgcctccagatcgtctccc 294

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*
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21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	294	100.0	294	14	US-10-001-254-5
2	294	100.0	1383	14	US-10-001-254-15
3	294	100.0	2817	10	US-09-966-451-3
4	294	100.0	2817	14	US-10-001-254-27
5	294	100.0	2817	16	US-10-630-399-3
6	293.4	99.5	1383	9	US-09-795-595-2
7	293.4	99.5	1383	10	US-09-759-595-2
8	293.4	99.5	1383	10	US-09-833-790-149
9	204.4	69.5	1542	9	US-09-795-595-4
10	204.4	69.5	1542	10	US-09-759-595-4
11	151.8	51.6	31000	10	US-09-966-451-10
12	151.8	51.6	31000	16	US-10-630-399-10

13	137.6	46.8	211	14	US-10-001-254-25	Sequence 25, Appl
14	137.6	46.8	470	16	US-10-242-535A-26096	Sequence 26096, A
15	137.6	46.8	470	16	US-10-085-783A-26096	Sequence 26096, A
16	104.8	35.6	408	11	US-09-969-034-428	Sequence 428, App
17	43.2	14.7	256493	13	US-10-087-192-1000	Sequence 1000, Ap
18	42.6	14.5	1694	18	US-10-422-522-27	Sequence 27, Appl
19	42.6	14.5	2378	18	US-10-357-930-23166	Sequence 23166, A
20	42.6	14.5	2378	18	US-10-357-930-29035	Sequence 29035, A
21	40.4	13.7	2024	9	US-09-895-752-51	Sequence 51, Appl
22	40.4	13.7	2024	9	US-09-887-586A-51	Sequence 51, Appl
23	40.4	13.7	2024	9	US-09-903-012-51	Sequence 51, Appl
24	40.4	13.7	2024	10	US-09-900-797-51	Sequence 51, Appl
25	40.4	13.7	2024	11	US-09-893-820-51	Sequence 51, Appl
26	39.6	13.5	628	18	US-10-468-488-12	Sequence 12, Appl
27	37	12.6	399	18	US-10-674-124A-9403	Sequence 9403, Ap
28	37	12.6	126413	13	US-10-087-192-1831	Sequence 1831, Ap
29	36	12.2	2000	9	US-09-938-842A-4518	Sequence 4518, Ap
30	36	12.2	2000	11	US-09-938-842A-4518	Sequence 4518, Ap
31	35	11.9	2703	16	US-10-282-122A-40657	Sequence 40657, A
32	34.6	11.8	504	18	US-10-425-115-154005	Sequence 154005, A
33	34.4	11.7	131673	18	US-10-723-860-4432	Sequence 4432, Ap
34	33.8	11.5	3879	16	US-10-282-122A-27393	Sequence 27393, A
35	33.8	11.5	22684	10	US-09-960-870-2	Sequence 2, Appl1
36	33.8	11.5	22684	10	US-09-960-858-2	Sequence 2, Appl1
37	33.8	11.5	22684	16	US-10-251-668-2	Sequence 2, Appl1
38	33.8	11.5	580073	15	US-10-205-220-1	Sequence 1, Appl1
39	33.6	11.4	1250	16	US-10-425-114-13505	Sequence 13505, A
40	33.6	11.4	1450	18	US-10-425-115-181981	Sequence 181981, A
41	33.6	11.4	2349	10	US-09-769-787-287	Sequence 287, App
42	33.6	11.4	2393	8	US-08-961-527-90	Sequence 90, Appl
43	33.6	11.4	2393	16	US-10-158-844-90	Sequence 90, Appl
44	33.4	11.4	548	18	US-10-723-860-5341	Sequence 5341, Ap
45	33.2	11.3	899	14	US-10-198-846-7068	Sequence 7068, Ap

ALIGNMENTS

RESULT 1
US-10-001-254-5
; Sequence 5, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sung Hyung
; APPLICANT: Roch, Wilfred
; APPLICANT: Stenmer-Liwen, Frank
; TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 294
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(294)
US-10-001-254-5
Query Match 100.0%; Score 294; DB 14; Length 294;
Best Local Similarity 100.0%; Pred. No. 5; 4e-75;
Matches 294; Conservative 0; Mismatches 0; Gaps 0;

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QY 1 ACATATGTCGCTGCTCAATGTTGACTAATTAGGAAGCTGTCAATTTTATGATCCT 60
DB 1 ACATATGTCGCTGCTCAATGTTGACTAATTAGGAAGCTGTCAATTTTATGATCCT 60
QY 61 CAAGAAGATGGAAGAAGTTAGCTGTAAGCTAATTAACCATCTGTGTGATGATATAC 120
DB 61 CAAGAAGATGGAAGAAGTTAGCTGTAAGCTAATTAACCATCTGTGTGATGATATAC 120
QY 121 AATCAGTTTCACATAAGAGATTGTAAGCACTTCAATCTGGAAGAAAGTCCACTTCT 180
DB 121 AATCAGTTTCACATAAGAGATTGTAAGCACTTCAATCTGGAAGAAAGTCCACTTCT 180
QY 181 GAATTACTGTTGACTGGGGGACCAACAATTCACAGTTGTGATCTTGTGATCTTTTG 240
DB 181 GAATTACTGTTGACTGGGGGACCAACAATTCACAGTTGTGATCTTGTGATCTTTTG 240
QY 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCCGAGATGCTGTTCC 294
DB 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCCGAGATGCTGTTCC 294
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RESULT 2

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US-10-001-254-15
; Sequence 15, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sug Hyung
; APPLICANT: Roch, Wilfred
; APPLICANT: Stenmer-Liwen, Frank
; TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1383
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1380)
US-10-001-254-15
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Query Match 100.0%; Score 294; DB 14; Length 1383;
Best Local Similarity 100.0%; Pred. No. 1.1e-74;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ACATATGTCGCTGCTCAATGTTGACTAATTAGGAAGCTGTCAATTTTATGATCCT 60
DB 25 ACATATGTCGCTGCTCAATGTTGACTAATTAGGAAGCTGTCAATTTTATGATCCT 84
QY 61 CAAGAAGATGGAAGAAGTTAGCTGTAAGCTAATTAACCATCTGTGTGATGATATAC 120
DB 85 CAAGAAGATGGAAGAAGTTAGCTGTAAGCTAATTAACCATCTGTGTGATGATATAC 144
QY 121 AATCAGTTTCACATAAGAGATTGTAAGCACTTCAATCTGGAAGAAAGTCCACTTCT 180
DB 145 AATCAGTTTCACATAAGAGATTGTAAGCACTTCAATCTGGAAGAAAGTCCACTTCT 204
QY 181 GAATTACTGTTGACTGGGGGACCAACAATTCACAGTTGTGATCTTGTGATCTTTTG 240
DB 205 GAATTACTGTTGACTGGGGGACCAACAATTCACAGTTGTGATCTTGTGATCTTTTG 264
QY 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCCGAGATGCTGTTCC 294
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DB 265 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCCGAGATGCTGTTCC 318
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RESULT 3

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US-09-966-451-3
; Sequence 3, Application US/09966451
; Publication No. US20030087856A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freiler
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESSION
; FILE REFERENCE: RUS-0324
; CURRENT APPLICATION NUMBER: US/09/966,451
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)...(1432)
US-09-966-451-3
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Query Match 100.0%; Score 294; DB 10; Length 2817;
Best Local Similarity 100.0%; Pred. No. 1.5e-74;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ACATATGTCGCTGCTCAATGTTGACTAATTAGGAAGCTGTCAATTTTATGATCCT 60
DB 74 ACATATGTCGCTGCTCAATGTTGACTAATTAGGAAGCTGTCAATTTTATGATCCT 133
QY 61 CAAGAAGATGGAAGAAGTTAGCTGTAAGCTAATTAACCATCTGTGTGATGATATAC 120
DB 134 CAAGAAGATGGAAGAAGTTAGCTGTAAGCTAATTAACCATCTGTGTGATGATATAC 193
QY 121 AATCAGTTTCACATAAGAGATTGTAAGCACTTCAATCTGGAAGAAAGTCCACTTCT 180
DB 194 AATCAGTTTCACATAAGAGATTGTAAGCACTTCAATCTGGAAGAAAGTCCACTTCT 253
QY 181 GAATTACTGTTGACTGGGGGACCAACAATTCACAGTTGTGATCTTGTGATCTTTTG 240
DB 254 GAATTACTGTTGACTGGGGGACCAACAATTCACAGTTGTGATCTTGTGATCTTTTG 313
QY 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCCGAGATGCTGTTCC 294
DB 314 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCCGAGATGCTGTTCC 367
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RESULT 4

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US-10-001-254-27
; Sequence 27, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sug Hyung
; APPLICANT: Roch, Wilfred
; APPLICANT: Stenmer-Liwen, Frank
; TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
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LENGTH: 2817
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (50) ... (1429)
US-10-001-254-27

Query Match 100.0%; Score 294; DB 14; Length 2817;
Best Local Similarity 100.0%; Pred. No. 1.5e-74;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGCGCGCTCCTCAATGTTGAGTAATTAAGAGCTGTGAGATTATTTATGATCCT 60
DB 74 ACATATGCGCGCTCCTCAATGTTGAGTAATTAAGAGCTGTGAGATTATTTATGATCCT 133
QY 61 CAAGAAGATGGAAGATTAGCTGTGACCTTAATAAAACCATCTGTGATGATGATAC 120
DB 134 CAAGAAGATGGAAGATTAGCTGTGACCTTAATAAAACCATCTGTGATGATGATAC 193
QY 121 AATGAGTTTCATPAAGAGATTGGAAGCATTAATCTGCAAGAAAAAGTCCACTTCT 180
DB 194 AATGAGTTTCATPAAGAGATTGGAAGCATTAATCTGCAAGAAAAAGTCCACTTCT 253
QY 181 GAATTACTGTTTGACTGGGCGACCAAAATTCACAGTTGATCTTGTGATCTTTTG 240
DB 254 GAATTACTGTTTGACTGGGCGACCAAAATTCACAGTTGATCTTGTGATCTTTTG 313
QY 241 ATCCAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTTTCC 294
DB 314 ATCCAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTTTCC 367

RESULT 5
US-10-630-399-3
Sequence 3, Application US/10630399
Publication No. US20040019009A1
GENERAL INFORMATION:
APPLICANT: Susan M. Freiler
TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESSION
FILE REFERENCE: RUS-0324
CURRENT APPLICATION NUMBER: US/10/630,399
CURRENT FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: US/09/966,451
PRIOR FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 3
LENGTH: 2817
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (50) ... (1429)
US-10-630-399-3

Query Match 100.0%; Score 294; DB 16; Length 2817;
Best Local Similarity 100.0%; Pred. No. 1.5e-74;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGCGCGCTCCTCAATGTTGAGTAATTAAGAGCTGTGAGATTATTTATGATCCT 60
DB 74 ACATATGCGCGCTCCTCAATGTTGAGTAATTAAGAGCTGTGAGATTATTTATGATCCT 133
QY 61 CAAGAAGATGGAAGATTAGCTGTGACCTTAATAAAACCATCTGTGATGATGATAC 120
DB 134 CAAGAAGATGGAAGATTAGCTGTGACCTTAATAAAACCATCTGTGATGATGATAC 193
QY 121 AATGAGTTTCATPAAGAGATTGGAAGCATTAATCTGCAAGAAAAAGTCCACTTCT 180
DB 194 AATGAGTTTCATPAAGAGATTGGAAGCATTAATCTGCAAGAAAAAGTCCACTTCT 253
QY 181 GAATTACTGTTTGACTGGGCGACCAAAATTCACAGTTGATCTTGTGATCTTTTG 240

DB 254 GAATTACTGTTTGACTGGGCGACCAAAATTCACAGTTGATCTTGTGATCTTTTG 313
QY 241 ATCCAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTTTCC 294
DB 314 ATCCAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTTTCC 367

RESULT 6
US-09-795-595-2
Sequence 2, Application US/09795595
Publication No. US20020039423A1
GENERAL INFORMATION:
APPLICANT: Wesche, Holger
APPLICANT: Li, Shyun
APPLICANT: Tularik Inc.
TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
FILE REFERENCE: 018781-003910US
CURRENT APPLICATION NUMBER: US/09/795,595
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1383
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human IL-1 receptor-associated kinase 4 (IRAK-4)
OTHER INFORMATION: cDNA
NAME/KEY: CDS
LOCATION: (1) ... (1383)
OTHER INFORMATION: human IRAK-4
US-09-795-595-2

Query Match 99.5%; Score 292.4; DB 9; Length 1383;
Best Local Similarity 99.7%; Pred. No. 3.2e-74;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACATATGCGCGCTCCTCAATGTTGAGTAATTAAGAGCTGTGAGATTATTTATGATCCT 60
DB 25 ACATATGCGCGCTCCTCAATGTTGAGTAATTAAGAGCTGTGAGATTATTTATGATCCT 84
QY 61 CAAGAAGATGGAAGATTAGCTGTGACCTTAATAAAACCATCTGTGATGATGATAC 120
DB 85 CAAGAAGATGGAAGATTAGCTGTGACCTTAATAAAACCATCTGTGATGATGATAC 144
QY 121 AATGAGTTTCATPAAGAGATTGGAAGCATTAATCTGCAAGAAAAAGTCCACTTCT 180
DB 145 AATGAGTTTCATPAAGAGATTGGAAGCATTAATCTGCAAGAAAAAGTCCACTTCT 204
QY 181 GAATTACTGTTTGACTGGGCGACCAAAATTCACAGTTGATCTTGTGATCTTTTG 240
DB 205 GAATTACTGTTTGACTGGGCGACCAAAATTCACAGTTGATCTTGTGATCTTTTG 264
QY 241 ATCCAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTTTCC 294
DB 265 ATCCAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTTTCC 318

RESULT 7
US-09-759-595-2
Sequence 2, Application US/09759595
Publication No. US20030059916A1
GENERAL INFORMATION:
APPLICANT: Wesche, Holger
APPLICANT: Li, Shyun
APPLICANT: Tularik Inc.
TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
FILE REFERENCE: 018781-003910US
CURRENT APPLICATION NUMBER: US/09/759,595
CURRENT FILING DATE: 2001-01-13

; PRIOR APPLICATION NUMBER: US 60/176,395
 ; PRIOR FILING DATE: 2000-01-13
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 1383
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human IL-1 receptor-associated kinase 4 (IRAK-4)
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1383)
 ; OTHER INFORMATION: human IRAK-4
 ; US-09-759-595-2

Query Match 99.5%; Score 292.4; DB 10; Length 1383;
 Best Local Similarity 99.7%; Pred. No. 3.2e-74;
 Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACATATGCGCTGCTCCTCAATGTTGACTAATTAGAGAGCTGCAGATTTTATGATCCT 60
 DB 25 ACATATGCGCTGCTCCTCAATGTTGACTAATTAGAGAGCTGCAGATTTTATGATCCT 84
 QY 61 CAAGAAGATGAGAGAGAGTTAGCTGTAGCTATTAAAAACCATCTGTGATGATGATAC 120
 DB 85 CAAGAAGATGAGAGAGAGTTAGCTGTAGCTATTAAAAACCATCTGTGATGATGATAC 144
 QY 121 AATCAGTTTCACATTAAGAGATTTGAGCACTTAATCTGAAAAAGTCCCACTTCT 180
 DB 145 AATCAGTTTCACATTAAGAGATTTGAGCACTTAATCTGAAAAAGTCCCACTTCT 204
 QY 181 GAATTAAGTTTGAAGTGGGACCAAAATGCAAGTTGGATCTTGGATCTTTG 240
 DB 205 GAATTAAGTTTGAAGTGGGACCAAAATGCAAGTTGGATCTTGGATCTTTG 264
 QY 241 ATCCAAATGAATTTTTTCTCTGCGAGTCTTTTCTCCAGATCTGTTCCC 294
 DB 265 ATCCAAATGAATTTTTTCTCTGCGAGTCTTTTCTCCAGATCTGTTCCC 318

RESULT 8
 ; US-09-833-790-149
 ; Sequence 149, Application US/09833790
 ; Patent No. US20020068288A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Wang, Tonglong
 ; APPLICANT: Secrist, Heather
 ; APPLICANT: Mohamach, Radoch
 ; APPLICANT: Indrias, Carol Y.
 ; APPLICANT: Fan, Liqun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.512
 ; CURRENT APPLICATION NUMBER: US/09/833,790
 ; CURRENT FILING DATE: 2001-04-11
 ; NUMBER OF SEQ ID NOS: 440
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 149
 ; LENGTH: 501
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(501)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-833-790-149

Query Match 82.2%; Score 241.6; DB 9; Length 501;
 Best Local Similarity 97.3%; Pred. No. 1.1e-59;
 Matches 288; Conservative 0; Mismatches 4; Indels 4; Gaps 4;

QY 1 ACATATGCGCTGCTCCTCAATGTTGACTAATTAGAGAGCTGCAGATTTTATGATCCT 60
 DB 45 ACATATGCGCTGCTCCTCAATGTTGACTAATTAGAGAGCTGCAGATTTTATGATCCT 104
 QY 61 CAAGAAGATGAGAGAGAGTTAGCTGTAGCTATTAAAAACCATCTGTGATGATGATAC 120
 DB 105 CAAGAAGATGAGAGAGAGTTAGCTGTAGCTATTAAAAACCATCTGTGATGATGATAC 164
 QY 121 AATCAGTTTCACATTAAGAGATTTGAGCACTTAATCTGAAAAAGTCCCACTTCT 179
 DB 165 AATCAGTTTCACATTAAGAGATTTGAGCACTTAATCTGAAAAAGTCCCACTTCT 223
 QY 180 TGATTAAGTTTGAAGTGGGACCAAAATGCAAGTTGGATCTTGGATCTTT 238
 DB 224 TGATTAAGTTTGAAGTGGGACCAAAATGCAAGTTGGATCTTGGATCTTT 283
 QY 239 TGATTAAGTTTGAAGTGGGACCAAAATGCAAGTTGGATCTTGGATCTTT 294
 DB 284 TGATTAAGTTTGAAGTGGGACCAAAATGCAAGTTGGATCTTGGATCTTT 338

RESULT 9
 ; US-09-795-595-4
 ; Sequence 4, Application US/09795595
 ; Publication No. US20020039423A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mesche, Holger
 ; APPLICANT: Li, Shyun
 ; APPLICANT: Tularek Inc.
 ; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
 ; FILE REFERENCE: 018781-003910US
 ; CURRENT APPLICATION NUMBER: US/09/795,595
 ; CURRENT FILING DATE: 2001-01-11
 ; PRIOR APPLICATION NUMBER: US 60/176,395
 ; PRIOR FILING DATE: 2000-01-13
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 1542
 ; TYPE: DNA
 ; ORGANISM: Mus sp.
 ; FEATURE:
 ; OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4)
 ; NAME/KEY: CDS
 ; LOCATION: (163)..(1542)
 ; OTHER INFORMATION: murine IRAK-4
 ; US-09-795-595-4

Query Match 69.5%; Score 204.4; DB 9; Length 1542;
 Best Local Similarity 81.0%; Pred. No. 1.1e-48;
 Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 ACATATGCGCTGCTCCTCAATGTTGACTAATTAGAGAGCTGCAGATTTTATGATCCT 60
 DB 187 ACATATGCGCTGCTCCTCAATGTTGACTAATTAGAGAGCTGCAGATTTTATGATCCT 246
 QY 61 CAAGAAGATGAGAGAGAGTTAGCTGTAGCTATTAAAAACCATCTGTGATGATGATAC 120
 DB 247 CAAGAAGATGAGAGAGAGTTAGCTGTAGCTATTAAAAACCATCTGTGATGATGATAC 306
 QY 121 AATCAGTTTCACATTAAGAGATTTGAGCACTTAATCTGAAAAAGTCCCACTTCT 180
 DB 307 AATCAGTTTCACATTAAGAGATTTGAGCACTTAATCTGAAAAAGTCCCACTTCT 366
 QY 181 GAATTAAGTTTGAAGTGGGACCAAAATGCAAGTTGGATCTTGGATCTTT 240
 DB 367 GAATTAAGTTTGAAGTGGGACCAAAATGCAAGTTGGATCTTGGATCTTT 426
 QY 241 ATCCAAATGAATTTTTTCTCTGCGAGTCTTTTCTCCAGATCTGTTCCC 294
 DB 427 ATCCAAATGAATTTTTTCTCTGCGAGTCTTTTCTCCAGATCTGTTCCC 480


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RESULT 10
US-09-759-595-4
; Sequence 4, Application US/09759595
; Publication No. US20030059916A1
; GENERAL INFORMATION:
; APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT APPLICATION NUMBER: US/09/759,595
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 60/176,395
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4)
; NAME/KEY: CDS
; LOCATION: (163)..(1542)
; OTHER INFORMATION: murine IRAK-4
; US-09-759-595-4

Query Match      69.5%; Score 204.4; DB 10; Length 1542;
Best Local Similarity 81.0%; Pred. No. 1.1e-48;
Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 ACATATGTGCGCTGCTCAATGTTGAGCTAATTAAGAAAGCTGTGAGATTTATTGATCT 60
DB 187 ACATACATAGCAACCTTAATGTGGGATCTTGAAGAGCTGTGGAATTTATTGATCT 246
QY 61 CAAGAAGATGGAAGAAATTAGCTGTAGCTATTAAAAACATCTGTGATGATAGATAC 120
DB 247 CAAGAAGGTGGAAGAAATTAGCACTAGCTATCAAAAAAGCCGTCCGGGACAGACGATAC 306
QY 121 AATGATTTCACTATAGAGATTTGAAGCATTTACTTCAAACTGAAAAAGTCCCACTTCT 180
DB 307 AATGATTTCACTATAGAGATTTGAAGCATTTACTTCAAGCCGGAGAGAGCCCACTTCT 366
QY 181 GAATTAAGTGTGAGCTGGGGACCAAAATTGACAGTTGTGATCTTTGATCTTTTG 240
DB 367 GAATGCTGTGAGCTGGGGACCAAGCACTGACAGTTGGGACCTTTGTGATCTTACTG 426
QY 241 ATCCAAATGAATTTTGTCTGCTCGAGTCTTTTGTCTCCAGATGCTGTTCCC 294
DB 427 GTCCAGATGAGCTGTTTGTCCCGCCGCACTCTCTGCTGCGGATGCGGTTCCC 480

RESULT 11
US-09-966-451-10
; Sequence 10, Application US/09966451
; Publication No. US20030087856A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freiler
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRES
; FILE REFERENCE: RTS-0324
; CURRENT APPLICATION NUMBER: US/09/966,451
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 10
; LENGTH: 31000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
```

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US-09-966-451-10
Query Match      51.6%; Score 151.8; DB 10; Length 31000;
Best Local Similarity 95.7%; Pred. No. 7.9e-33;
Matches 156; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 123 TCAGTTTCACATAGAGATTTTGAAGCATTAATTCAAACTGAAAAAGTCCCACTTCTGA 182
DB 12953 TTACTTACTTTTAAGAGATTTGAAGCATTAATTCAAACTGAAAAAGTCCCACTTCTGA 13012
QY 183 ATTACTGTTGAGCTGGGGACCAAAATTGACAGTTGTGATCTTTGATCTTTTGAT 242
DB 13013 ATTACTGTTGAGCTGGGGACCAAAATTGACAGTTGTGATCTTTGATCTTTTGAT 13072
QY 243 CCAAAATGAATTTTGTCTGCTGAGATCTTTGCTCCAGAT 285
DB 13073 CCAAAATGAATTTTGTCTGCTGAGATCTTTGCTCCAGAT 13115

RESULT 12
US-10-630-399-10
; Sequence 10, Application US/10630399
; Publication No. US2004001909A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freiler
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRES
; FILE REFERENCE: RTS-0324
; CURRENT APPLICATION NUMBER: US/10/630,399
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/966,451
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 10
; LENGTH: 31000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

Query Match      51.6%; Score 151.8; DB 16; Length 31000;
Best Local Similarity 95.7%; Pred. No. 7.9e-33;
Matches 156; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 123 TCAGTTTCACATAGAGATTTTGAAGCATTAATTCAAACTGAAAAAGTCCCACTTCTGA 182
DB 12953 TTACTTACTTTTAAGAGATTTGAAGCATTAATTCAAACTGAAAAAGTCCCACTTCTGA 13012
QY 183 ATTACTGTTGAGCTGGGGACCAAAATTGACAGTTGTGATCTTTGATCTTTTGAT 242
DB 13013 ATTACTGTTGAGCTGGGGACCAAAATTGACAGTTGTGATCTTTGATCTTTTGAT 13072
QY 243 CCAAAATGAATTTTGTCTGCTGAGATCTTTGCTCCAGAT 285
DB 13073 CCAAAATGAATTTTGTCTGCTGAGATCTTTGCTCCAGAT 13115

RESULT 13
US-10-001-254-25
; Sequence 25, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sug Hyung
; APPLICANT: Roth, Wilfred
; APPLICANT: Steiner-llewen, Frank
; TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; CURRENT FILING DATE: 2001-11-15
```

PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 211
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(177)
US-10-001-254-25

Query Match 46.8%; Score 137.6; DB 14; Length 211;
Best Local Similarity 97.2%; Pred. No. 1e-29;
Matches 140; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACATATGCGCGCTCAATGTTGACTAATTAGAACTGTGAGATTTTATGATCCT 60
DB 25 ACATATGCGCGCTCAATGTTGACTAATTAGAACTGTGAGATTTTATGATCCT 84
QY 61 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTAAAAACCATCTGGTATGATAGATAC 120
DB 85 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTAAAAACCATCTGGTATGATAGATAC 144
QY 121 AATCAGTTTCACATAAGAGATTT 144
DB 145 AATCAGTTTCACATAAGATGCTGT 168

RESULT 14

US-10-242-535A-26096
Sequence 26096, Application US/10242535A
Publication No. US2004001363A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 26096
LENGTH: 470
TYPE: DNA
ORGANISM: Human
US-10-242-535A-26096

Query Match 46.8%; Score 137.6; DB 16; Length 470;
Best Local Similarity 97.2%; Pred. No. 1.5e-29;
Matches 140; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACATATGCGCGCTCAATGTTGACTAATTAGAACTGTGAGATTTTATGATCCT 60
DB 139 ACATATGCGCGCTCAATGTTGACTAATTAGAACTGTGAGATTTTATGATCCT 198
QY 61 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTAAAAACCATCTGGTATGATAGATAC 120
DB 139 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTAAAAACCATCTGGTATGATAGATAC 258
QY 121 AATCAGTTTCACATAAGAGATTT 144

DB 259 AATCAGTTTCACATAAGATGCTGT 282

RESULT 15

US-10-085-783A-26096
Sequence 26096, Application US/10085783A
Publication No. US20040037841A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 26096
LENGTH: 470
TYPE: DNA
ORGANISM: Human
US-10-085-783A-26096

Query Match 46.8%; Score 137.6; DB 16; Length 470;
Best Local Similarity 97.2%; Pred. No. 1.5e-29;
Matches 140; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACATATGCGCGCTCAATGTTGACTAATTAGAACTGTGAGATTTTATGATCCT 60
DB 139 ACATATGCGCGCTCAATGTTGACTAATTAGAACTGTGAGATTTTATGATCCT 198
QY 61 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTAAAAACCATCTGGTATGATAGATAC 120
DB 199 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTAAAAACCATCTGGTATGATAGATAC 258
QY 121 AATCAGTTTCACATAAGAGATTT 144
DB 259 AATCAGTTTCACATAAGATGCTGT 282

Search completed: January 12, 2005, 07:07:01
Job time : 2055 secs

C	27	C	32	10.9	9834	4	US-08-956-171E-37	Sequence 37, Appl
C	26	C	32	10.9	3012	4	US-09-919-039-167	Sequence 167, Appl
C	25	C	32	10.9	3012	4	US-09-976-594-482	Sequence 422, Appl
C	24	C	32	11.0	2274	4	US-09-107-532A-3535	Sequence 3535, Appl
C	23	C	32.2	11.0	4402	4	US-09-484-970B-135	Sequence 135, Appl
C	22	C	32.4	11.0	98844	4	US-09-791-211-10	Sequence 10, Appl
C	21	C	32.4	11.1	1737	4	US-09-248-796A-2516	Sequence 3449, Appl
C	20	C	32.6	11.1	2971	4	US-09-710-279-3449	Sequence 3, Appl
C	19	C	32.6	11.1	1728	4	US-09-096-734A-1	Sequence 1, Appl
C	18	C	32.6	11.2	202001	4	US-09-734-674A-3	Sequence 3, Appl
C	17	C	32.8	11.2	477	4	US-09-513-999C-32039	Sequence 12039, Appl
C	16	C	33	11.2	640681	4	US-09-790-988-1	Sequence 1, Appl
C	15	C	33.2	11.3	654	4	US-09-248-796A-236	Sequence 236, Appl
C	14	C	33.6	11.4	2393	4	US-08-961-527-90	Sequence 50, Appl
C	13	C	33.6	11.4	711	4	US-09-583-012B-1653	Sequence 1653, Appl
C	12	C	33.8	13.0	580073	4	US-08-545-828D-1	Sequence 1, Appl
C	11	C	38.2	13.7	267	4	US-08-543-681A-1549	Sequence 1549, Appl
C	10	C	40.4	13.7	2024	4	US-09-900-797-51	Sequence 51, Appl
C	9	C	40.4	13.7	2024	4	US-09-903-012B-51	Sequence 51, Appl
C	8	C	40.4	13.7	2024	4	US-09-885-752-51	Sequence 51, Appl
C	7	C	40.4	13.7	2024	4	US-09-887-586A-51	Sequence 51, Appl
C	6	C	40.4	13.7	2024	4	US-09-398-395A-51	Sequence 51, Appl
C	5	C	40.4	13.7	2024	3	US-09-601-091-1	Sequence 3, Appl
C	4	C	40.4	13.7	1879	3	US-09-601-091-1	Sequence 1, Appl
C	3	C	151.8	51.6	31000	4	US-09-966-451-10	Sequence 10, Appl
C	2	C	294	100.0	833	4	US-09-166-350-10	Sequence 10, Appl
C	1	C	294	100.0	833	4	US-09-166-350-10	Sequence 10, Appl

C	28	32	10.9	9834	4	US-08-781-986A-37	Sequence 37, Appl
	29	31.8	10.8	1545	4	US-09-710-279-2681	Sequence 2681, Ap
	30	31.8	10.8	1557	3	US-09-134-001C-1614	Ap Sequence 1614, Ap
	31	31.8	10.8	2807	4	US-09-620-312D-120	Sequence 120, App
C	32	31.8	10.8	3247	4	US-09-710-279-3771	Sequence 3771, Ap
	33	31.8	10.8	166976	4	US-08-915-421B-1	Sequence 1, Appl
	34	31.8	10.8	166976	4	US-09-692-570-1	Sequence 1, Appl
	35	31.4	10.7	832	4	US-09-621-976-2813	Sequence 2813, Ap
C	36	31.4	10.7	3320	4	US-09-710-279-3337	Sequence 3383, Ap
	37	31.4	10.7	3454	4	US-09-710-279-3398	Sequence 3398, Ap
C	38	31.4	10.7	4045	4	US-09-710-279-3329	Sequence 3329, Ap
	39	31.4	10.7	12720	1	US-08-403-866-11	Sequence 11, Appl
	40	31	10.5	2126	2	US-08-545-745-1	Sequence 1, Appl
C	41	30.8	10.5	224	4	US-09-513-999C-11151	Sequence 11151, A
	42	30.8	10.5	708	4	US-09-248-796A-6765	Sequence 6765, Ap
	43	30.8	10.5	1056	4	US-09-134-000C-1031	Sequence 1031, Ap
	44	30.8	10.5	1161	4	US-09-976-599-423	Sequence 423, App
	45	30.8	10.5	1550	4	US-09-427-501-1	Sequence 1, Appl

ALIGNMENTS

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```

Query Match	100.0%;	Score 294;	DB 4;	Length 833;
Best Local Similarity	100.0%;	Pred. No. 1.1e-82;		
Matches 294; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

Qy	1	ACATATGTCGCTGCTCATAATGTGGACTAATATGGAAGCTGCAGATTTATTTATGATCT	60
Db	74	AATATATGTCGCTGCCTCAATGTTGGAATAATTGGAAGCTGTCAGATTTATATGATCT	133
Qy	61	CAGAAGATGTGAAGAAGTTAGCTGTACTCTAATTAACCAATCATGTGGATGATAGATAC	126
Db	134	CAGAAGATGTGAAGAAGTTAGCTGTACTCTAATTAACCAATCATGTGGATGATAGATAC	195
Qy	121	AATCAGTTTCACATTAAGAGATTTGAAAGCATTTACTTCAACCTGAAAAAGTCCACTTCT	180
Db	194	AATCAGTTTCACATTAAGAGATTTGAAAGCATTTACTTCAACCTGAAAAAGTCCACTTCT	253
Qy	181	GAAATACGTCTTGACTGAGGACCACAAAATTGCACAGTGGTGATCTTGATGATCTTTTG	240
Db	254	GAAATACGTCTTGACTGAGGACCACAAAATTGCACAGTGGTGATCTTGATGATCTTTTG	313
Qy	241	ATCCAAAATGAATTTTTTGTCTCTGCCAGTCTTTTGTCTCCCAAGTGTGTTCCT	294
Db	314	ATCCAAAATGAATTTTTTGTCTCTGCCAGTCTTTTGTCTCCCAAGTGTGTTCCT	367

	Query Match	Best Local Similarity	Matches	Score	DB	Length	Mismatches	Indels	Gaps
Qy	123	TCAGTTCACATAGAGAGATTGAGCATTTACTTCAAACTGGAAAAAGATCCACTTCTGA	182	51.6%	151.8	4	95.7%	0	0
Db	12953	TTACTCTCTTTTAGAGGAAATTTGAGCATTTCTCAAACTGGAAAAAGATCCCACTTCTGA	13012	95.7%	2.3e-37	7	0	0	0

RESULT 5
 US-09-601-091-3
 ; Sequence 3, Application US/09601091
 ; Patent No. 6342380
 ; GENERAL INFORMATION:
 ; APPLICANT: Colby, S. M. et al.
 ; TITLE OF INVENTION: Germacrene C Synthase Gene of *Lycopersicon Esculentum*
 ; FILE REFERENCE: 4630-55758
 ; CURRENT APPLICATION NUMBER: US/09/601,091
 ; CURRENT FILING DATE: 2000-09-19
 ; PRIOR APPLICATION NUMBER: PCT/US99/02133
 ; PRIOR FILING DATE: 1999-02-02
 ; PRIOR APPLICATION NUMBER: US 60/773,579
 ; PRIOR FILING DATE: 1998-02-02
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: Patentlin Ver. 2.0
 ; SEQ ID NO 3

LENGTH: 2024
TYPE: DNA
ORGANISM: Lycopersicon esculentum
FEATURE:
NAME/KEY: CDS
LOCATION: (32)..(1678)
US-09-601-091-3

Query Match 13.7%; Score 40.4; DB 3; Length 2024;
Best Local Similarity 50.5%; Pred. No. 0.0066;
Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 45 AGATTATTTAGTCTCAAGAGATGAGAGAGATTAGCTAGCTATTAAAAACATC 104
DB 754 AGAGCTTAGTATCTTACAGGTGCTGGAAGATTGATTTGCAATTAATATCCATA 813
QY 105 TGGTGATGATGATACATCACTGTTTCACTAAGAGATTGAGATTACTTCAAACTGG 164
DB 814 TGCAAGACAGAGTGTGATGATGTTACTTCTGATATTAGAGGTATTTGAGCCAAA 873
QY 165 AAAAGTCCCACTTGTGAATTACTGTTGACTGGGGCACCAATTTGACAGTTGGTGA 224
DB 874 ATATAGTGTGCGAGAAAATGATGACAAAGTACTCACTGACCTTCATTATTGACGA 933
QY 225 TCTTGTGATCTTT 238
DB 934 CACTTTGATGCTT 947

RESULT 6
US-09-398-395A-51
Sequence 51, Application US/09398395A
Patent No. 6468772
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 64687721, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/398,395A
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 51
LENGTH: 2024
TYPE: DNA
ORGANISM: Lycopersicon esculentum
FEATURE:
NAME/KEY: CDS
LOCATION: (32)..(1675)
OTHER INFORMATION: VENT germacrene C synthase
US-09-398-395A-51

Query Match 13.7%; Score 40.4; DB 4; Length 2024;
Best Local Similarity 50.5%; Pred. No. 0.0066;
Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
QY 45 AGATTATTTAGTCTCAAGAGATGAGAGAGATTAGCTAGCTATTAAAAACATC 104
DB 754 AGAGCTTAGTATCTTACAGGTGCTGGAAGATTGATTTGCAATTAATATCCATA 813
QY 105 TGGTGATGATGATACATCACTGTTTCACTAAGAGATTGAGATTACTTCAAACTGG 164
DB 814 TGCAAGACAGAGTGTGATGATGTTACTTCTGATATTAGAGGTATTTGAGCCAAA 873
QY 165 AAAAGTCCCACTTGTGAATTACTGTTGACTGGGGCACCAATTTGACAGTTGGTGA 224

DB 874 ATATAGTGTGCGAGAAAATGATGACAAAGTACTCACTGACCTTCATTATTGACGA 933
QY 225 TCTTGTGATCTTT 238
DB 934 CACTTTGATGCTT 947

RESULT 7
US-09-887-586A-51
Sequence 51, Application US/09887586A
Patent No. 6495354
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 64953541, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/887,586A
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 51
LENGTH: 2024
TYPE: DNA
ORGANISM: Lycopersicon esculentum
FEATURE:
NAME/KEY: CDS
LOCATION: (32)..(1675)
OTHER INFORMATION: VENT germacrene C synthase
US-09-887-586A-51

Query Match 13.7%; Score 40.4; DB 4; Length 2024;
Best Local Similarity 50.5%; Pred. No. 0.0066;
Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
QY 45 AGATTATTTAGTCTCAAGAGATGAGAGAGATTAGCTAGCTATTAAAAACATC 104
DB 754 AGAGCTTAGTATCTTACAGGTGCTGGAAGATTGATTTGCAATTAATATCCATA 813
QY 105 TGGTGATGATGATACATCACTGTTTCACTAAGAGATTGAGATTACTTCAAACTGG 164
DB 814 TGCAAGACAGAGTGTGATGATGTTACTTCTGATATTAGAGGTATTTGAGCCAAA 873
QY 165 AAAAGTCCCACTTGTGAATTACTGTTGACTGGGGCACCAATTTGACAGTTGGTGA 224
DB 874 ATATAGTGTGCGAGAAAATGATGACAAAGTACTCACTGACCTTCATTATTGACGA 933
QY 225 TCTTGTGATCTTT 238
DB 934 CACTTTGATGCTT 947

RESULT 8
US-09-895-752-51
Sequence 51, Application US/09895752
Patent No. 6559297
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 65592971, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/895,752
CURRENT FILING DATE: 2001-06-29

```
;; PRIOR APPLICATION NUMBER: 09/398,395
;; PRIOR FILING DATE: 1999-09-17
;; PRIOR APPLICATION NUMBER: 60/100,993
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/130,628
;; PRIOR FILING DATE: 1999-04-22
;; PRIOR APPLICATION NUMBER: 60/150,262
;; PRIOR FILING DATE: 1999-08-23
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 51
;; LENGTH: 2024
;; TYPE: DNA
;; ORGANISM: Lycopersicon esculentum
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (32)...(1675)
;; OTHER INFORMATION: VFNT germacrene C synthase
US-09-895-752-51
```

```
Query Match      13.7%; Score 40.4; DB 4; Length 2024;
Best Local Similarity 50.5%; Pred. No. 0.0066;
Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
```

```
Oy 45 AGATTTTATGATCCTCAAGAGATGAGAGAGATTAGCTGATTTAAACCATC 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 754 AGAGCTTAGATGATCTTACAGAGTGCGGAGAAAGATTGGCAATTAATCCATA 813
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 105 TGGTGATGATGATACATCAATCAGTTTCACATTAAGAGATTGAGCATTCCTCAACTG 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 814 TCGAAGAGACAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 873
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 165 AAAAGTCCCACTTGAATTAATCTGTTGACTGGGGACCAAAATGACAGTGGTGA 224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 874 ATATAGTCGTGCAGAAAATGATGACAAAGTACTGACCTCCATATTGACGA 933
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 225 TCTTGTGATCTT 238
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 934 CACTTTGATGCTT 947
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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```
RESULT 9
US-09-903-012B-51
; Sequence 51, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6569656, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 2024
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)...(1675)
; OTHER INFORMATION: VFNT germacrene C synthase
US-09-903-012B-51
```

Query Match 13.7%; Score 40.4; DB 4; Length 2024;

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Best Local Similarity 50.5%; Pred. No. 0.0066;
Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

Oy 45 AGATTTTATGATCCTCAAGAGATGAGAGATTAGCTGATTTAAACCATC 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 754 AGAGCTTAGATGATCTTACAGAGTGCGGAGAAAGATTGGCAATTAATCCATA 813
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 105 TGGTGATGATGATACATCAATCAGTTTCACATTAAGAGATTGAGCATTCCTCAACTG 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 814 TCGAAGAGACAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 873
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 165 AAAAGTCCCACTTGAATTAATCTGTTGACTGGGGACCAAAATGACAGTGGTGA 224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 874 ATATAGTCGTGCAGAAAATGATGACAAAGTACTGACCTCCATATTGACGA 933
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 225 TCTTGTGATCTT 238
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 934 CACTTTGATGCTT 947
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 10
US-09-900-797-51
; Sequence 51, Application US/0990797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6645762, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 2024
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)...(1675)
; OTHER INFORMATION: VFNT germacrene C synthase
US-09-900-797-51
```

Query Match 13.7%; Score 40.4; DB 4; Length 2024;
Best Local Similarity 50.5%; Pred. No. 0.0066;
Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

```
Oy 45 AGATTTTATGATCCTCAAGAGATGAGAGATTAGCTGATTTAAACCATC 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 754 AGAGCTTAGATGATCTTACAGAGTGCGGAGAAAGATTGGCAATTAATCCATA 813
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 105 TGGTGATGATGATACATCAATCAGTTTCACATTAAGAGATTGAGCATTCCTCAACTG 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 814 TCGAAGAGACAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 873
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 165 AAAAGTCCCACTTGAATTAATCTGTTGACTGGGGACCAAAATGACAGTGGTGA 224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 874 ATATAGTCGTGCAGAAAATGATGACAAAGTACTGACCTCCATATTGACGA 933
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 225 TCTTGTGATCTT 238
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 934 CACTTTGATGCTT 947
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 11

	Query Match	Similarity	11.5%	Score 33.8	DB 4	Length 580073
	Best Local	Similarity	53.4%	Pred. No. 9		
	Matches	71	Conservative	0	Mismatches 62	Indels 0
					Gaps	0
Qy	143	TTGAAGCATTACTTCGAACTGGAAGAAAGTCCCACTCTGAAATTAATGTTGACTGGGGCA	202			
Db	431703	TTGAAGCATTGTGTAACCAAAACCAAACTCTGATGTAATCATTAATTTGACAGATTG	431644			
Qy	203	CCACAAATTGCACAGTGGTGATCTTTGGATTTTGGATCCAAATGAAATTTTTGGCTC	262			
Db	431643	TTAATCGCTACTCAATTAATCTATAGTTGATCTGAAACACAAAATCAATTGTGAGAG	431584			
Qy	263	CTGGAGTCTTTT	275			
Db	431583	CTAAGTCTTAAT	431571			

1 GENERAL INFORMATION:
2 APPLICANT: Charles Kunsch
3 TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
4 NUMBER OF SEQUENCES: 391
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: Human Genome Sciences, Inc.
7 STREET: 9410 Key West Avenue
8 CITY: Rockville
9 STATE: Maryland
10 COUNTRY: USA
11 ZIP: 20850
12
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Diskette, 3.5 inch, 1.4Mb storage
15 COMPUTER: HP Vectra 486/33
16 OPERATING SYSTEM: MSDOS version 6.2
17 SOFTWARE: ASCII Text
18
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/961,527
21
22 FILING DATE:
23 CLASSIFICATION: 424
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER:
26
27 FILING DATE:
28
29 ATTORNEY/AGENT INFORMATION:
30

NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 2393 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-90

Query Match 11.4%; Score 33.6; DB 4; Length 2393;
Best Local Similarity 48.9%; Pred. No. 0.97; Mismatches 94; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 37 AAGCTGTCAGATTTTATTTGATCTCAGAGAGATGAGAGAGATTAGCTAGCTATTAA 96
DB 1113 AACCTTTAGTACCAACGAGACTAAAGAGCTGCAACAAAGAGATATTCCTATTAG 1054
QY 97 AAACCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 156
DB 1053 ATAGGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 994
QY 157 CAACTGGAAGAAAGTCCCACTTCTGATTAATGATGATGATGATGATGATGATGAT 216
DB 993 GTTACTCTAAGAAATATCTGCTAATTTGCAATATATGAGAGACTTAACACTTGACA 934
QY 217 GTTG 220
DB 933 AATG 930

RESULT 15
US-09-248-796A-236
; Sequence 236, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248, 796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 236
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-236

Query Match 11.3%; Score 33.2; DB 4; Length 654;
Best Local Similarity 51.3%; Pred. No. 0.74; Mismatches 73; Indels 0; Gaps 0;
Matches 77; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 85 GTAGCTATTAAAAAACCATCTGATGATGATGATGATGATGATGATGATGATGATGAT 144
DB 226 GTAGCATCAAGACACGACGACCCGTTAAGTTGATGATGATGATGATGATGATGAT 285
QY 145 GAAGCATTTACTCAAACTGAGAAAAGTCCCACTTCTGATTAATGATGATGATGATGAT 204
DB 286 GCAAAATTATGAGAGATTGAGAAAGCCCACTTGAATGATGATGATGATGATGATGAT 345
QY 205 ACAATTTGACAGTGGTGGATCTTGAT 234
DB 346 AAGTATGATCTCAATGTTGTTACCAAGAT 375

Search completed: January 12, 2005, 05:40:47
Job time : 90 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 03:33:48 ; Search time 1934 Seconds

(without alignments)
5539,442 Million cell updates/sec

Title: US-10-001-254-5

Perfect score: 294
Sequence: 1 acatactgtgcgtcctcaaa.....tgcctccagatcgtctccc 294

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST.*
1: gb_esc1.*
2: gb_esc2.*
3: gb_esc3.*
4: gb_esc4.*
5: gb_esc5.*
6: gb_esc6.*
7: gb_esc7.*
8: gb_esc8.*
9: gb_esc9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	294	100.0	859	4	BG164491 602342026
2	292.4	99.5	811	4	BG164438 602642772
3	273.2	92.9	821	7	CK459029 923479 WA
4	267.2	90.9	719	2	BF696981 602130160
5	262	89.1	402	2	BE482619 168463 BA
6	262	89.1	666	7	CN788062 4122347 B
7	261	88.8	1383	9	AY418791 Homo sapi
8	258.4	87.9	1383	9	AY418792 Pan trogl
9	220	74.8	541	4	BG691069 340084 BA
10	205.4	69.9	313	4	BM151935 TCBAPE11
11	204.4	69.5	503	6	CA538859 C0272801
12	204.4	69.5	598	5	BOS52228 H4014C09
13	204.4	69.5	637	2	BB660378 BB660378
14	204.4	69.5	637	2	BB613447 BB613447
15	204.4	69.5	638	6	BT721552 BT721552
16	204.4	69.5	663	6	BY726858 BY726858
17	204.4	69.5	676	6	BB613167 BB613167
18	204.4	69.5	1161	3	AKO20397 Mus muscu
19	204.4	69.5	2481	3	AKO28837 Mus muscu
20	204.4	69.5	2810	5	AKO29028 Mus muscu
21	202.8	67.6	575	5	BK522921 BK522921
22	198.8	62.0	265	2	AM436511 76774 MAR
23	182.4	62.0	507	2	BB866698 BB866698
24	182.2	62.0	1286	9	AY418793 Mus muscu

25	181.4	61.7	524	2	AM106160
26	163.2	55.5	453	2	BB860349
27	154.2	52.4	686	2	CN066297 F20_Ag2_P
28	154.2	52.4	711	7	CN067840 K20_Ag2_P
29	154.2	52.4	775	7	CN061000 A22_Ag2_P
30	154.2	52.4	782	7	CN064552 Ag2_P_L2
31	147.6	50.2	852	5	BU209111 603950834
32	144.4	49.1	600	1	AJ453616 AJ453616
33	144.4	49.1	670	1	AJ447581 AJ447581
34	141.8	48.2	417	7	CO780006 BL0088_H0
35	139.8	47.6	540	1	AL699213 DKFZP686K
36	139.6	47.5	505	2	BE482323 168064 BA
37	139.4	47.4	606	1	AL647125 AL647125
38	139.2	47.3	625	9	CE224557 ligR-g88-
39	137.6	46.8	284	1	AA114228 znf505.1
40	137.6	46.8	753	6	CD654941 AGENCOURT
41	137.6	46.8	783	7	CF596589 AGENCOURT
42	134	45.6	576	2	BF238344 601904613
43	125.8	42.0	270	2	BE845841 233716 BA
44	123.4	42.0	664	4	BU035962 BU035962
45	114.4	38.9	599	4	BU691338 BU691338

ALIGNMENTS

RESULT 1
LOCUS BG164491 859 bp mRNA linear EST 06-FEB-2001
DEFINITION 602342026F1 NIH_MGC_89 Homo sapiens CDNA clone IMAGE:4452055 5',
mRNA sequence.

ACCESSION BG164491.1 GI:12671194
VERSION BG164491.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 859)
NIH-MGC http://mgc.ncbi.nlm.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strauberg, Ph.D.
COMMENT Email: cgabs-remail.nih.gov
Tissue Procurement: ARCC

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov

Plate: LHAM10240 row: d column: 08
High quality sequence stop: 634.
Location/Qualifiers
1..859
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4452055"
/issue_type="hypermethylation, cell line"
/lab host="DH10B (phage-resistant)"
/clone_11b="NIH_MGC_89"
/note="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

FEATURES

source

ORIGIN

Query Match 100.0%; Score 294; DB 4; Length 859;
Best Local Similarity 100.0%; Pred. No. 1e-70;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGTCGCTGCTCAATGTTGAATTAAGAGCTGCAGATTTTATGATCCT 60
 Db 59 ACATATGTCGCTGCTCAATGTTGAATTAAGAGCTGCAGATTTTATGATCCT 118
 QY 61 CAAGAAGATGAGAGAGTTAGCTGTAGCTATTAATAAACATCTGTATGATGATATAC 120
 Db 119 CAAGAAGATGAGAGAGTTAGCTGTAGCTATTAATAAACATCTGTATGATGATATAC 178
 QY 121 AATCAGTTTCACATAGAGAGATTTGAACATTAATCTTCAACTGGAAAAAGTCCACTTCT 180
 Db 179 AATCAGTTTCACATAGAGAGATTTGAACATTAATCTTCAACTGGAAAAAGTCCACTTCT 238
 QY 181 GAATTAAGTGTGATCTGGGACCAACAATTTGACAGTTGGATCTTGTGATCTTTTG 240
 Db 239 GAATTAAGTGTGATCTGGGACCAACAATTTGACAGTTGGATCTTGTGATCTTTTG 298
 QY 241 ATCCAAATGAAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTCTCC 294
 Db 299 ATCCAAATGAAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTCTCC 352

RESULT 2
 BG616438 811 bp mRNA linear EST 18-APR-2001
 LOCUS 602642772F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4773760 5',
 DEFINITION mRNA sequence.

ACCESSION BG616438
 VERSION BG616438.1 GI:13667809
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Eutheria; Primates; Catarrhini; Homiidae; Homo.
 JOURNAL NIH-MGC http://mgc.nci.nih.gov/
 COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1645 row: P column: 17
 High quality sequence start: 3
 High quality sequence stop: 613.
 Location/Qualifiers

FEATURES
 source 1..811

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4773760"
 /tissue_type="embryonal carcinoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_1ib="NIH MGC 61"
 /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
 SfiI (ggcgccctcgcc); Site_2: SfiI (ggccatcagcc);
 Double-stranded cDNA was prepared from cell line RNA. 5'
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGGCATTATGGCC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGCGCGGCGCGCATG-dt(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
 library."

ORIGIN
 Query Match 99.5%; Score 292.4; DB 4; Length 811;

Best Local Similarity 99.7%; Pred. No. 2.8e-70;
 Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ACATATGTCGCTGCTCAATGTTGAATTAAGAGCTGCAGATTTTATGATCCT 60
 Db 77 ACATATGTCGCTGCTCAATGTTGAATTAAGAGCTGCAGATTTTATGATCCT 136
 QY 61 CAAGAAGATGAGAGAGTTAGCTGTAGCTATTAATAAACATCTGTATGATGATATAC 120
 Db 137 CAAGAAGATGAGAGAGTTAGCTGTAGCTATTAATAAACATCTGTATGATGATATAC 196
 QY 121 AATCAGTTTCACATAGAGAGATTTGAACATTAATCTTCAACTGGAAAAAGTCCACTTCT 180
 Db 197 AATCAGTTTCACATAGAGAGATTTGAACATTAATCTTCAACTGGAAAAAGTCCACTTCT 256
 QY 181 GAATTAAGTGTGATCTGGGACCAACAATTTGACAGTTGGATCTTGTGATCTTTTG 240
 Db 257 GAATTAAGTGTGATCTGGGACCAACAATTTGACAGTTGGATCTTGTGATCTTTTG 316
 QY 241 ATCCAAATGAAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTCTCC 294
 Db 317 ATCCAAATGAAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTCTCC 370

RESULT 3
 CK459029 821 bp mRNA linear EST 14-JAN-2004
 LOCUS 923479 MARC 4P1G Sus scrofa cDNA 5', mRNA sequence.
 DEFINITION CK459029
 ACCESSION CK459029.1 GI:40830310
 VERSION CK459029.1 GI:40830310
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa

REFERENCE
 AUTHORS Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 TITLE Smith, T.P.L., Preking, B.A., Ford, J.J., Vallee, J.L., Wise, T.A.,
 JOURNAL Nonhuman, D.J., Wray, J.E. and Keefe, J.W.
 COMMENT Porcine EST collection using a normalized library constructed from
 embryos representing early developmental stages
 Unpublished (2003)
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Plate: TWM8032 row: K column: 23
 Seq primer: GTAATACAGCTCACTATAGG.
 Location/Qualifiers

FEATURES
 source 1..821

/organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_1ib="MARC 4P1G"
 /note="Vector: pCDNA3.1; Site_1: EcoRI; Site_2: NotI;
 library made with combined RNA from day-10, day-13,
 day-15, day-25, and day-30 whole embryos."

ORIGIN
 Query Match 92.9%; Score 273.2; DB 7; Length 821;
 Best Local Similarity 95.6%; Pred. No. 5.9e-65;
 Matches 281; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 1 ACATATGTCGCTGCTCAATGTTGAATTAAGAGCTGCAGATTTTATGATCCT 60
 Db 233 ACATATGTCGCTGCTCAATGTTGAATTAAGAGCTGCAGATTTTATGATCCT 292

Oy		61	CAGAAGATGGAACAGTTAGCTGTAGCTATTAAAAACAATCGGGATGATGATAC	120
Dd		293	CAGAGAGATGAGAGATTACGATAGCTATTAAAAACAATCTGGTGAATGACAGATAC	352
Oy		121	AATCAGTTTCATATAGAGAGATTGGAMGCATTACTTCAAACGTGAAAAAGTCCCACTTCT	180
Dd		353	AACGAGTTTCATATAGAGAGATTGAGACATTACTTCAAACGTGAAAAAGTCCCACTTGT	412
Oy		181	GAATTACTGTTTTGACTGGGGCACCAAAATTGCACAGTTGGTATCTTGAGATCTTTTG	240
Dd		413	GAATTACTGTTTTGACTGGGGCACCAAAATTGCACAGTTGGGATCTTGAGATCTTTTG	472
Oy		241	ATCCAAATGATTTTTTGTCTCCGGGAGTCTTTGTCCCAAGATCGTGTCCC	294
Dd		473	GTCGAAAATGAGTTTTTTGCCCTGCACAGTCTTTGTCTTCAGATGCTGTTCCC	526
RESULT 4				
BF696981				
LOCUS		BF696981	719 bp	mRNA linear EST 22-DEC-2000
DEFINITION		602130160P1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287014 5'		
		mRNA sequence.		
ACCESSION		BF696981		
VERSION		BF696981.1	GI:11982389	
KEYWORDS		EST.		
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE		1 (bases 1 to 719)		
AUTHORS		NIH-MGC http://mgc.nci.nih.gov/.		
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL		Unpublished (1999)		
COMMENT		Contact: Robert Strausberg, Ph.D.		

```

Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: L10CM124 row: g column: 15
High quality sequence stop: 632.
Location/Qualifiers
1. 719
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGS:4287014"
/tissue_type="Primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1fb="NH_MGC_56"
/note="Organ: brain; Vector: pDNR-L1B (Clontech); Site_1:
SfiI (ggcgccgcgcgc); Site_2: SfiI (ggccatcggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGAGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGAGCGCGGACATG-dT(130)BN-3'
(Where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

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Query Match	90.9%	Score 267.2	DB 2	Length 719
Best Local Similarity	98.3%	Pred. No. 2.7e-63		
Matches 291	Conservative 0	Mismatches 5	Indels 2	Gaps 2
Qy	1	ACATATGTCGCGCTGCTCAATGTTGGACTAATTAGGAGCTGCAGATTTTATTGATCTT	60	
Db	92	ACATATGCGCCCTGCTCCTAATGTTGGACTAATTAGGAGCTGCAGATTTTATTGATCTT	151	

QY 61 CAAGAAGATGGAAACACTTGGCTGCTAGCTATTAAAAAACCATCTGGTGATGATGATAC 120
Db 152 CAGGAAGATGGAAACAGTTAGCTGCTAGCTATTAAAAAACCATCTGGTGATGATGATAC 211
QY 121 AATCAGTTTCCATATAGGAGATTTTGACCATTTCTTCAAACTGGAAGAAAGTCCACTTCT 180
Db 212 AATCAGTTTCCATATAGGAGATTTGAACATTTACTTCAAACTGGAAGAAAGTCCACTTCT 271
QY 181 GAATTACT-GTTTGACTGGGGGACACAAATTGCAACAGTTGGTGATCTTTGGATCTTTT 239
Db 272 GAATTACTGGTTTGACTGGGGGACACAAATTGCAACAGTTGGTGATCTGGTGATCTTTT 331
QY 240 GATCCAAATGAATTT-TTGGCTCTGGGAGCTCTTTGGTCTCCAGATGCTTTCC 294
Db 332 GATCCAAATGAATTTGTTGGCTCTCTGCAAGCTTTTGGTCTCCAGATGCTTTCC 387

RESULT 5					
BE482619					
LOCUS	BE482619	402 bp	mRNA	linear	EST 27-MAR-2003
DEFINITION	1694463 BARC 5BOV Bos taurus CDNA 5', mRNA sequence.				
ACCESSION	BE482619				
VERSION	BE482619.1	GI:9602152			
KEYWORDS	EST.				
SOURCE	Bos taurus (cow)				
ORGANISM	Bos taurus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eumammalia; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.				
REFERENCE	1 (bases 1 to 402)				
AUTHORS	Sonstegard,T., Capuco,A.V., White,J., Van Tassell,C.P., Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,D.E., Wells,K.D. and Quackenbush,J.				
TITLE	Analysis of bovine mammary gland EST and functional annotation of the Bos taurus gene index				
JOURNAL	Mamm. Genome 13	(7),	373-379	(2002)	
MEDLINE	22135956				
PubMed	12140684				
COMMENT	Contact: Sonstegard TS				

```

USA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@jpsl.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 11 row: F column: 7
Seq primer: ATTAGGTGACACTGATG.
Location/Qualifiers
1..402
/oranism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/cisue_type="pooled"
/lab_host="DH10B"
/clone_id="BARC 5BOV"
/note="Vector: PCMV SPOR6, Site 1: NotI; Site 2: SalI;
library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

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Query Match	89.1%	Score 262;	DB 2;	Length 402;
Best Local Similarity	93.2%	Pred. No. 6.7e-62;		
Matches 274; Conservative	0;	Mismatches 20;	Indels 0;	Gaps 0;
1	ACATATGTGGCGCTCCATGATGTGGACTAATTGGAAGCTGTGAGATTTATTTGATCCT	60		

89.1%; Score 262; DB 7; Length 666;

QY 1 ACATATGTGCGTGCCCTCAATGTTGGACTAATTAGGACCTGTCCAGATTTTAAATTGATCCT 60

Db 25 ACATATGTGCGTGCTCAATGTTGACTAATTAGGAAAGCTGTCCAGATTTTAAATTGATCCT 84

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Qy 61 CAAGAAGATGAGAGATTAGCTGTATTAATAAACCATCTGGNGATGATGATAC 120
Db 85 CAGAGAGATGAGAGAGATTAGCTGTATTAATAAACCATCTGGNGATGATGATAC 144
Qy 121 AATCAGTTTCACATAGAGAGATTGGAAGCATTTACTTCAAACTGGAAGAAAGTCCCACTTCT 180
Db 145 AATCAGTTTCACATAGAGAGATTGGAAGCATTTACTTCAAACTGGAAGAAAGTCCCACTTCT 204
Qy 181 GAATTACTGTTTACCTGGGACCAACAATTGCAAGTGTGATCTTTGGATCTTTTG 240
Db 205 GAATTACTGTTTACCTGGGACCAACAATTGCAAGTGTGATCTTTGGATCTTTTG 264
Qy 241 ATCCAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTTCCC 294
Db 265 ATCCAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTTCCC 318

RESULT 8
AY418792 1383 bp DNA linear GSS 17-DEC-2003
LOCUS Pan troglodytes IRAK4 gene, VIRtual TRANSCRIPT, partial sequence,
ACCESSION AY418792
VERSION AY418792.1 GI:39774752
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
1 (bases 1 to 1383)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Fertiera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
These sequences were made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
location/Qualifiers
1..1383
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/gene="IRAK4"
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ORIGIN
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Best Local Similarity 88.1%; Pred. No. 8.3e-61;
Matches 259; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 1 ACATATGTCGCTGCTCAATGTTGACTAATTAGAAAGCTGTGAGATTTTATGATCT 60
Db 25 ACATATGTCGCTGCTCAATGTTGACTAATTAGAAAGCTGTGAGATTTTATGATCT 84
Qy 61 CAAGAAGATGAGAGATTAGCTGTATTAATAAACCATCTGGNGATGATGATAC 120
Db 85 CAGAGAGATGAGAGAGATTAGCTGTATTAATAAACCATCTGGNGATGATGATAC 144
Qy 121 AATCAGTTTCACATAGAGAGATTGGAAGCATTTACTTCAAACTGGAAGAAAGTCCCACTTCT 180
Db 145 AATCAGTTTCACATAGAGAGATTGGAAGCATTTACTTCAAACTGGAAGAAAGTCCCACTTCT 204

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Qy 181 GAATTACTGTTTACCTGGGACCAACAATTGCAAGTGTGATCTTTGGATCTTTTG 240
Db 205 GAATTACTGTTTACCTGGGACCAACAATTGCAAGTGTGATCTTTGGATCTTTTG 264
Qy 241 ATCCAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTTCCC 294
Db 265 ATCCAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTTTNC 318

RESULT 9
BG691069 541 bp mRNA linear EST 27-MAR-2003
LOCUS 340084 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BG691069
VERSION BG691069.1 GI:13932889
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 541)
Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
Connor,B.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
and Quackenbush,J.
Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
22135956
12140684
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Belg. 200 Km 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@ipcl.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCTGAGTCAGCAGC
Plate: 100 row. B column: 15
Seq primer: ATTTAGCTGACACTATG.
FEATURES
location/Qualifiers
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/organism="Bos taurus"
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/db_xref="taxon:9913"
/cisue_type="pooled"
/lab_host="DH10B"
/clone_lib="BARC 5BOV"
/notes="Vector: pCMV SPORTE; Site 1: NotI; Site 2: SalI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

ORIGIN
Query Match 74.8%; Score 220; DB 4; Length 541;
Best Local Similarity 93.9%; Pred. No. 3.2e-50;
Matches 229; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 51 TATTGATCTTCAGAGAGATGAGAGATTAGCTGTATTAATAAACCATCTGCTGA 110
Db 1 TATTGATCTTCAGAGAGATGAGAGATTAGCTGTATTAATAAACCATCTGCTGA 60
Qy 111 TGATAGTACATCAGTTTACATAGAGAGATTGGAAGCATTTCTTCAACTGGAAG 170
Db 61 TGATAGTACATCAGTTTACATAGAGAGATTGGAAGCATTTCTGCAAAATGGAAAG 120
Qy 171 TCCCACTTCTGAATTTACTGTTTGACTGGGACCAACAATTGCAAGTGTGATCTTGT 230

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Db 121 CCCACGCTGTGAGTACTGTTGACTGGGGACCAACAATTGCACAGTTGGATCTTGT 180
 Oy 231 GGATCTTTGATCCAAATGAAATTTTTCCTCTCGAGTCTTTTGTCCAGATGCTGT 290
 Db 181 GGATTTTGTGTCAAAAGATTTTTCCTCGAGTCTTTTGTACACAGATGCTGT 240
 Oy 291 TCCC 294
 Db 241 ACCC 244

RESULT 10
 BM151935 313 bp mRNA linear EST 30-NOV-2001
 LOCUS TCBAP11457 Pediatric pre-B cell acute lymphoblastic leukemia
 DEFINITION Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBAP1145, mRNA
 sequence.

ACCESSION BM151935.1 GI:17175815
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 313)
 AUTHORS Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R., Jr.,
 Gunaratne,P.H., Munzy,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.
 TITLE Pediatric Leukemia cDNA Sequencing Project (2001)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Dr. Judith F. Margolin
 Texas Children's Cancer Center and Human Genome Sequencing Center
 at Baylor College of Medicine
 1102 Bates, MC3-3320 Houston, TX 77030, USA
 Tel: 832-824-4536
 Fax: 832-825-4038
 Email: clones@ccc.org
 Seq primer: M13 primer.

FEATURES
 source location/Qualifiers

1..313
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="TCBAP1145"
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 /cell_type="pre-B cell"
 /dev_stage="pediatric 2 years"
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 /clone_1lb="Pediatric pre-B cell acute lymphoblastic
 leukemia Baylor-HGSC project-TCBA"
 /note="Vector: lambda pSB, Site 1: BamHI, Site 2: EcoRI;
 first strand cDNA was primed with an anchored
 xhoI-oligo(dT) primer [5'GAGAGCTCAGCGCGCAGAGAGAG(T)VN
 3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand
 was primed with a BamHI-dc primer
 [5'AGAGAGCTCGATCCGCGCGCCCAATTAATATAT(C) 3'].
 Double-stranded cDNA was then digested with BamHI and XhoI
 and directionally cloned into the digested with BamHI and XhoI
 lambda pSB vector. Library went through one round of
 normalization. Library was constructed by Wei Yu at RIKEN
 of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
 Itoh M, Nagaoka S, Sasaki, Okazaki Y, Muramatsu M,
 Schneider C, Hayashizaki Y, High efficiency selection of
 full-length cDNA by improved biotinylated cap trapper.,
 NDA Res 4: 1, 61-6, Feb 28, 1997)"

ORIGIN

Query Match 69.9%; Score 205.4; DB 4; Length 313;
 Best Local Similarity 92.7%; Pred. No. 3.3e-46;
 Matches 215; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Oy 1 ACATATGGCGCTGCATGTTGAGTACTGTTGACTGGGGACCAACAATTGCACAGTTGGATCTTGT 60
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 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 77 ACATATGGCGCTGCCTCATGTTGAGTACTGAGTAATTAGGAAGCTGCAGATTTTATGATCCT 136
 Oy 61 CAAGAAGATGGAAGAAGTACTGATGATTAATAAACAATCTGGTGAATAGATAC 120
 Db 137 CAAAGAGATGGAAGAAGTACTGATGATTAATAAACAATCTGGTGAATAGATAC 196
 Oy 121 AATCAGTTTCACATAGAGATTTTGAAGCATTTCTCAATCTGGAAGAAAGTCCACTCT 180
 Db 197 AATCAGTTTCACATAGAGATTTTGAAGCATTTCTCTTCAATCTGGAAGAAAGTCCACTCT 256
 Oy 181 GAATTCGTTTGAATCTGGGGACCAACAATTGCACAGTTGATCTTGTGG 232
 Db 257 GAATTCGTTTGAATCTGGGGACCAACAATTGCACAGTTGATCTTGTGG 308

RESULT 11
 CA538859 503 bp mRNA linear EST 19-NOV-2002
 LOCUS C0272B01-SN NIA Mouse 7.5-dpc Whole Embryo cDNA Library (long) Mus
 DEFINITION musculus cDNA clone NIA: C0272B01 IMAGE:30017484 5', mRNA sequence.
 ACCESSION CA538859
 VERSION EST.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 503)
 AUTHORS Luo,A.Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Tanaka,T., Lim,M.K.,
 TITLE Systematic Analyses of NIA Mouse 7.5-dpc Whole Embryo cDNA Library
 JOURNAL Unpublished (2001)
 COMMENT Other ESTs: C0272B01-3
 Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov
 Plate: C0272 row: B column: 01
 Seq primer: M13 Reverse
 High quality sequence stop: 503
 POLYA=No.

FEATURES
 source location/Qualifiers

1..503
 /organism="Mus musculus"
 /mol_type="mRNA"
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 /db_xref="nlaEST:C0272B01-5N"
 /db_xref="taxon:10090"
 /clone="NIA:C0272B01 IMAGE:30017484"
 /tissue_type="whole embryo including extraembryonic
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 /dev_stage="7.5-days postcoitum"
 /lab_host="DH10B"
 /clone_1lb="NIA Mouse 7.5-dpc Whole Embryo cDNA Library
 (long)"
 /note="Vector: pSPORT1 (Invitrogen); Site 1: SalI, Site 2:
 NotI; Mouse cDNA project by the Laboratory of Genetics,
 National Institute on Aging (NIA), Intramural Research
 Program, NIH (http://1gsun.grc.nia.nih.gov/cDNA). This is
 a long-transcript enriched cDNA library (Ref. Genome Res.
 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
 extracted from a pool of four embryos at 7.5-days
 postcoitum. Double-stranded cDNAs were synthesized with an
 oligo(dT) primer (Invitrogen).
 5'-pCACTAGTCTTGATCGAGCGCGCTTTTCTTTTCTTTT-3' from
 7 ug of total RNA, treated with T4 DNA polymerase, and
 purified by ethanol-precipitation. The cDNAs were ligated
 to lone-linker IL-Sal4, purified by phenol/chloroform, and
 separated from free linkers by Centricon 100. Then, the
 cDNAs were amplified by long-range high fidelity PCR using
 Ex Tag polymerase (Takara) with a primer Sal4-S. The

Products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2 kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN

Query Match 69.5%; Score 204.4; DB 6; Length 503;
Best Local Similarity 81.0%; Pred. No. 6.8e-46;
Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 ACATATGCGCGCTGCTCAATCTTGGACTAATTAGAGCTGTCAAGTTTATTATCT 60
DB 192 ACATATGCGCGCTGCTCAATCTTGGACTAATTAGAGCTGTCAAGTTTATTATCT 251
QY 61 CAAGAGGATGGAAGAAATTAGCTAGCTATTAAAAACCATCTGTGATGATGATAC 120
DB 252 CAAGAGGATGGAAGAAATTAGCTAGCTATTAAAAACCATCTGTGATGATGATAC 311
QY 121 AATCAGTTTCATATAGAGATTTGAGCATTTCAACTGAAAAAGTCCACTTCT 180
DB 312 AATCAGTTTCATATAGAGATTTGAGCATTTCAACTGAAAAAGTCCACTTCT 371
QY 181 GAATTAAGTCTTTGACTGGGGCACCACAATTGCACAGTTGTGATCTTTGATCTTTG 240
DB 372 GAATTAAGTCTTTGACTGGGGCACCACAATTGCACAGTTGTGATCTTTGATCTTTG 431
QY 241 ATCCAAATGAATTTTGTCTCTCGAGTCTTTTGTCTCCAGATGCTGTCTCC 294
DB 432 GTCCAGATTGAGCTTTTGTCTCTCGAGTCTTTTGTCTCCAGATGCTGTCTCC 485

RESULT 12

B0552228

LOCUS

H4014C09-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone

B0552228 598 bp mRNA linear EST 20-JUN-2002

H4014C09-5', mRNA sequence.

B0552228.1 GI:21453114

EST.

Mus musculus (house mouse)

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 598)

VanBuren, V., Piao, Y., Dudekula, D., Qian, Y., Carter, M.G.,

Martin, P.R., Stagg, C.A., Bassey, U., Aiba, K., Hamatani, T.,

Kargul, G.J., Luo, A.G., Kelso, J., Hide, W. and Ko, M.S.H.

Assembly, verification, and initial annotation of NIA 7.4K mouse

cDNA clone set

Genome Res. 12 (12), 1999-2003 (2002)

JOURNAL

MEDLINE

PUBMED

COMMENT

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

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JOURNAL

MEDLINE

PUBMED

COMMENT

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

1. 598
/location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"

/clone="H4014C09"
/sex="mixed"
/dev_stage="mixed"
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clone is among a rearranged set of 7,407 clones from more
than 20 cDNA libraries."

ORIGIN

Query Match 69.5%; Score 204.4; DB 5; Length 598;
Best Local Similarity 81.0%; Pred. No. 7e-46;
Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 ACATATGCGCGCTGCTCAATCTTGGACTAATTAGAGCTGTCAAGTTTATTATCT 60
DB 176 ACATATGCGCGCTGCTCAATCTTGGACTAATTAGAGCTGTCAAGTTTATTATCT 235
QY 61 CAAGAGGATGGAAGAAATTAGCTAGCTATTAAAAACCATCTGTGATGATGATAC 120
DB 236 CAAGAGGATGGAAGAAATTAGCTAGCTATTAAAAACCATCTGTGATGATGATAC 295
QY 121 AATCAGTTTCATATAGAGATTTGAGCATTTCAACTGAAAAAGTCCACTTCT 180
DB 296 AATCAGTTTCATATAGAGATTTGAGCATTTCAACTGAAAAAGTCCACTTCT 355
QY 181 GAATTAAGTCTTTGACTGGGGCACCACAATTGCACAGTTGTGATCTTTGATCTTTG 240
DB 356 GAATTAAGTCTTTGACTGGGGCACCACAATTGCACAGTTGTGATCTTTGATCTTTG 415
QY 241 ATCCAAATGAATTTTGTCTCTCGAGTCTTTTGTCTCCAGATGCTGTCTCC 294
DB 416 GTCCAGATTGAGCTTTTGTCTCTCGAGTCTTTTGTCTCCAGATGCTGTCTCC 469

RESULT 13

BB660378

LOCUS

BB660378 RIKEN full-length enriched, 13 days embryo lung Mus

musculus cDNA clone D43042L21 5', mRNA sequence.

BB660378.1 GI:16494199

EST.

Mus musculus (house mouse)

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 610)

Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,

Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,

Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,

Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,

Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,

Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

Unpublished (2001)

Contact: Yoshihide Hayashizaki

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Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,

Watanabe, M., Yoneda, Y., Iehikawa, T., Ozawa, K., Tanaka, T.,

Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A.

and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
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Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamana, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

FEATURES

Location/Qualifiers

1. 610
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="D43004221"
/tissue_type="lung"
/dev_stage="13 days embryo"
/lab_host="DH10B"
/clone_1lb="RIKEN full-length enriched, 13 days embryo
lung"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGCGCGCGACACTGTTTCTTTTCTTTT 3']. cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5',
GAGAGAGAGATCTCGAGTTAATTAATTAATTCCTCCCTCC 3']. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda F1C I."

ORIGIN

Query Match 69.5%; Score 204.4; DB 2; Length 610;
Best Local Similarity 81.0%; Pred. No. 7e-46;
Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
1 ACATATGCGGCTGCTCAATGTTGACCTAATTAGAGAGCTGTGATTTTATGATCT 60
212 ACATATGCGGCTGCTCAATGTTGACCTAATTAGAGAGCTGTGATTTTATGATCT 271
61 CAAGAAGATGAGAGAGTTAGCTGATTTAAATCAATCTGGTATGATGATC 120
272 CAAGAAGGTTGAGAGAAATTAGAGAGTATCAAAAACCTCCGCGACAGACGATC 331
121 AATCGTTTCAATAGAGATTTGAGCATTCTTCAATGAGAAAAGTCCACTTCT 180
332 AATCGTTTCAATAGAGATTTGAGCATTCTTCAATGAGAAAAGTCCACTTCT 391
181 GAATATGTTTGAATGCGGCGACCAATATGACAGTTGGATCTTGTGATCTTTTG 240
392 GAATGCTGTTGATCTGGGCGACCAAGACTGACAGTTGGGACCTTGTGATCTTCTG 451
241 ATCCAAAATGATTTTGTCTCTCGAGTCTTTTGTCTCCAGATGCTGTTGCC 294
452 GTCCAGATTTGAGCTGTTGCCCCCGCACTCTCTGCTGCGGAGCGGATCGCTTCC 505

RESULT 14
BB613447
LOCUS BB613447 637 bp mRNA linear EST 26-OCT-2001

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BB613447 RIKEN full-length enriched, 10 day neonate skin Mus
musculus cDNA clone 4732482P03 5', mRNA sequence.
BB613447.1 GI:16454055

EST.
Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 637)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ichii, Y., Ito, M., Kawai, J.,
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ono, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)

Contact: Yoshihide Hayashizaki
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL:http://genome.gsc.riken.jp/
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wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watanuki, M., Yoneda, Y., Ishikawa, T., Oawa, K., Tanaka, T.,
Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format
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10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
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Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamana, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.

Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

FEATURES

source

Location/Qualifiers

1. 637

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="4732482P03"

/sex="mixed"

/tissue_type="skin"

/dev_stage="10 days neonate"

/lab_host="DH10B"

/clone_1lb="RIKEN full-length enriched, 10 day neonate
skin"

/note="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGATCTCGAGTTAATTAATTAATTCCTCCCTCC 3']. cDNA was

prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTTAAATTAATCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pluescript KS(+) after bulk excision from Lambda FLC I"

ORIGIN

Query Match 69.5%; Score 204.4; DB 2; Length 637;
Best Local Similarity 81.0%; Pred. No. 7.1e-46;
Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 ACATATGTCGGCTCCCTCAATGTTGAGTAAATGAGAGCTGTCAGATTTATTGATCTT 60
DB 193 ACATACATACCAACCTTAATGTTGGGAGTCTTAGAGAGCTGTCGATTTATTGATCTT 252
QY 61 CAAGAAGATGAGAGATGTTAGTGTGCTTAAATAAACAATGCTGATGATGATGATAC 120
DB 253 CAAGAAGGTTGAGAGATGAGATGAGTGTGCTTAAATAAACAATGCTGATGATGATGATAC 312
QY 121 AATCAGTTTCACATAGAGATTTGAAGCATTTCAACTGCAAAAAGTCCCACTTCT 180
DB 313 AATCAGTTTCATATAGAGATTTGAAGCATTTCAACTGCAAAAAGTCCCACTTCT 372
QY 181 GAATTAATCTGTTGACGCGGACCAACAATGTCAGATGTTGATCTTGGATCTTTTG 240
DB 373 GAACTGCTGTTGACGCGGACCAACAATGTCAGATGTTGATCTTGGATCTTTTG 432
QY 241 ATCCAAATGAAATTTTGTCTCCGAGTCTTTTGTCCCAAGATGCTGTTCCC 294
DB 433 GTCCAGATGAGCTGTTGTTGCCCCCGCACCTCTCTGCGAGATGCGTTCCC 486

RESULT 15

LOCUS BY721552 638 bp mRNA linear EST 17-DEC-2002
DEFINITION BY721552 RIKEN full-length enriched, adult male diencephalon Mus
musculus cDNA clone 9330209D03 5', mRNA sequence.

ACCESSION BY721552
VERSION BY721552.1 GI:27134669
KEYWORDS EST
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
1 (bases 1 to 638)

REFERENCE

AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Otsu, N., Saito, R., Suzuki, H., Yamataka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D. A., Quackenbush, J., Schiraldi, L. M., Kanapin, A., Matsuda, H.,
Batilov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,
Crotti, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
Gastaldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W. J., Petrea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
Sandelin, A., Schneider, C., Sempile, C. A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L. G., Wyszynski, B. A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arai, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Ichih, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Saitama-cho, Tsukuba, Ibaraki, 305-3858, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi, J., Aizawa, K., Akimura, T., Arai, K., Carninci, P.,
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numata, R., Ohno, M., Ohnaka, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, W.,
Takeda, Y., Waki, K., Watanabe, A., Yamashita, M. and Hayashizaki, Y.
Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
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sequencing pipeline with 384 multicapillary sequencer. Genome Res.
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Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
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cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES

SOURCE

1. 638
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="9330209D03"
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diencephalon"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN Division of Experimental Animal Research in Riken
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GAGAGAGATTCGAGTTAAATTAATTAATTAATCCCCCCCC 3'], cDNA was
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to Rot = 10.0 and subtraction to Rot = 185.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCGAGTTAAATTAATTAATCCCCCCCC 3'].
cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pluescript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
BamHI"

PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
 XX
 PS Claim 18; Page 173-174; 209pp; English.
 XX

The invention relates to an isolated polypeptide comprising a death domain (DD), death effector domain (DED) or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or NIDD (NGFR-interacting Death Domain), with a candidate binding agent and detecting the association of the domain and the candidate binding agent, by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or chemical crosslinking, nuclear magnetic resonance (NMR), mass spectroscopy (MS) and FPA. The invention is useful for modulating the level of a cell process such as cell proliferation, cell adhesion, cell immunoglobulin class switching, in particular apoptosis within a cell. Antibody specifically reactive with CTDD DD of C. trachomatis, C. muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the CTDD DD protein is useful for detecting a Chlamydia infection. The invention is useful for modulating the activity of oncogenic proteins, for treating a pathology caused by the oncogenic proteins and for treating bacterial infections by modulating the activity of bacterial proteins. The protein and antibody specific for it are useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases. The protein is useful for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense therapy and gene therapy. The present sequence is human IRAK4 DD cDNA

Sequence 294 BP; 84 A; 55 C; 62 G; 93 T; 0 U; 0 Other;

Query Match 100.0%; Score 294; DB 6; Length 294;
 Best Local Similarity 100.0%; Pred. No. 1.4e-77;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTATGTGGCGCTGCATATGTTGACATTAATGAGAGCTGCAGATTTTATGATCT 60
 DB 1 AACTATGTGGCGCTGCATATGTTGACATTAATGAGAGCTGCAGATTTTATGATCT 60
 QY 61 CAGAAGATGAGAAAGTTAGCTGTATTAATTAACATCTGGTGTATGATGATAC 120
 DB 61 CAGAAGATGAGAAAGTTAGCTGTATTAATTAACATCTGGTGTATGATGATAC 120
 QY 121 AATCAGTTTCACATTAAGAGATTGAAAGCATTAATCTGAAAGTCCACTTCT 180
 DB 121 AATCAGTTTCACATTAAGAGATTGAAAGCATTAATCTGAAAGTCCACTTCT 180
 QY 181 GAATTAAGTTGAGCTGGGACACCAAAATGACAGTGGATCTTGGATCTTTTG 240
 DB 181 GAATTAAGTTGAGCTGGGACACCAAAATGACAGTGGATCTTGGATCTTTTG 240
 QY 241 ATCCAAATGAATTTTCTCTCGAGATCTTTTCTCCAGATCTGTTCCC 294
 DB 241 ATCCAAATGAATTTTCTCTCGAGATCTTTTCTCCAGATCTGTTCCC 294

RESULT 2

AADS9056
 ID AADS9056 standard; cDNA; 294 BP.
 XX

AC AADS9056;

DT 18-DEC-2003 (first entry)

XX Human IRAK4 DD cDNA.

KW Human; death Domain; DD; death effector domain; DED; cell proliferation;
 KW Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
 KW neural growth factor receptor-interacting death domain; cell adhesion;
 KW vasotropic; microbial infection; inflammation; allograft rejection; CTDD;
 KW cell stress response; benign prostatic hypertrophy; antibacterial; NIDD;

KW apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
 KW neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;
 KW Keloid; interleukin-1 receptor-associated kinase; IRAK; gene; ss.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 CDS 1..294
 FT /tag= a
 FT /product= "Human IRAK4 DD protein"
 FT /note= "No start and stop codon"
 FT /partial

US2003049702-A1.

13-MAR-2003.

15-NOV-2001; 2001US-00001254.

17-NOV-2000; 2000US-00715893.

17-NOV-2000; 2000US-0367360P.

29-JUN-2001; 2001US-0301889P.

(REED/) REED J C.
 (GODZ/) GODZIK A.
 (PAWL/) PAWLOWSKI K.
 (PIOR/) FIORENTINO L.
 (LEBS/) LEE S H.
 (ROTH/) ROTH W.
 (STEN/) STENNER-LIEWEN F.

Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
 Stenner-Liewen F;
 PI

WPI; 2002-50022/53.
 P-PSDB; AAB38897.

PT New polypeptide comprising a death domain or death effector domain,
 PT useful for discovery of drugs that suppress infection, inflammation,
 PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
 XX

Claim 18; Page 33-34; 99pp; English.

The present invention provides novel death Domain (DD) and death effector domain (DED) proteins and nucleic acids encoding them. The invention also provides death domain containing protein such as Chlamydia trachomatis death domain containing protein (CTDD) DD and neural growth factor receptor-interacting death domain (NIDD) DD. The invention is useful for identifying a binding agent (e.g. protein or drug) that binds a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate binding agent and identifying an effective agent (e.g. protein or drug) that modulates the association of a DD, DED or NB-ARC domain with protein that binds the DD, DED or NB-ARC domain. The invention is also useful for modulating the level of cell process such as apoptosis, cell adhesion, cell proliferation, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching. DEDs and NB-ARC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are useful for discovery of drugs that suppress infection, autoimmunity, inflammation, allergy, allograft rejection, sepsis and other diseases. DD, DED or NB-ARC domain proteins are used to treat infection, allergy, autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis, inflammatory hyperplasia and smooth muscle cell proliferation in arteries following balloon angioplasty (restenosis). The invention is also used in antibody therapy and gene therapy. The present sequence is human interleukin-1 receptor-associated kinase (IRAK)-4 DD cDNA

Sequence 294 BP; 84 A; 55 C; 62 G; 93 T; 0 U; 0 Other;

Query Match 100.0%; Score 294; DB 6; Length 294;
 Best Local Similarity 100.0%; Pred. No. 1.4e-77;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGCGCGCTCCCTCAATGTTGACTAATAGGAAGCTGTGAGATTTTATGATCCT 60
 DB 1 ACATATGCGCGCTCCCTCAATGTTGACTAATAGGAAGCTGTGAGATTTTATGATCCT 60
 QY 61 CAAGAAGATGGAAGAAGTTAGCTGTGACTATTAATAAACCATCTGGTGTGATGATGATAC 120
 DB 61 CAAGAAGATGGAAGAAGTTAGCTGTGACTATTAATAAACCATCTGGTGTGATGATGATAC 120
 QY 121 AATAGTTTCACATAGAGAGATTGGAAGCATTAATCTGCAAAAGTGAAGAAAGTCCACTTCT 180
 DB 121 AATAGTTTCACATAGAGAGATTGGAAGCATTAATCTGCAAAAGTGAAGAAAGTCCACTTCT 180
 QY 181 GAATTACTGTTTGACTGGGACCAACAATTGACAGTTGGTGAATCTTGATCTTTTG 240
 DB 181 GAATTACTGTTTGACTGGGACCAACAATTGACAGTTGGTGAATCTTGATCTTTTG 240
 QY 241 ATCCAAATGAAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCCC 294
 DB 241 ATCCAAATGAAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCCC 294

RESULT 3

AAA09319
 ID AAA09319 standard; DNA; 833 BP.

AC AAA09319;

DT 10-AUG-2000 (first entry)

DE Human cancer associated antigen precursor DNA, clone NY-REN-64.

XX renal cancer; cancer associated antigen precursor; diagnosis; cytostatic;

KW 88.

OS Homo sapiens.

XX

XX

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XX

XX

SQ Sequence 833 BP; 273 A; 155 C; 179 G; 226 T; 0 U; 0 Other;

Query Match 100.0%; Score 294; DB 3; Length 833;

Best Local Similarity 100.0%; Pred. No. 1.9e-77;

Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGCGCGCTCCCTCAATGTTGACTAATAGGAAGCTGTGAGATTTTATGATCCT 60
 DB 74 ACATATGCGCGCTCCCTCAATGTTGACTAATAGGAAGCTGTGAGATTTTATGATCCT 133
 QY 61 CAAGAAGATGGAAGAAGTTAGCTGTGACTATTAATAAACCATCTGGTGTGATGATGATAC 120
 DB 134 CAAGAAGATGGAAGAAGTTAGCTGTGACTATTAATAAACCATCTGGTGTGATGATGATAC 193
 QY 121 AATAGTTTCACATAGAGAGATTGGAAGCATTAATCTGCAAAAGTGAAGAAAGTCCACTTCT 180
 DB 194 AATAGTTTCACATAGAGAGATTGGAAGCATTAATCTGCAAAAGTGAAGAAAGTCCACTTCT 253
 QY 181 GAATTACTGTTTGACTGGGACCAACAATTGACAGTTGGTGAATCTTGATCTTTTG 240
 DB 254 GAATTACTGTTTGACTGGGACCAACAATTGACAGTTGGTGAATCTTGATCTTTTG 313
 QY 241 ATCCAAATGAAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCCC 294
 DB 314 ATCCAAATGAAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCCC 367

RESULT 4

AAD40079
 ID AAD40079 standard; DNA; 1383 BP.

AC AAD40079;

DT 22-OCT-2002 (first entry)

DE Human IRAK4 gene #1.

XX

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XX

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XX

XX

XX

XX

XX

Key Location/Qualifiers
 CDS 1..1383
 /*tag= a
 /product= "Human IRAK4"

W0200240680-A2.

23-MAY-2002.

15-NOV-2001; 2001WO-US044844.

17-NOV-2000; 2000US-00715893.

29-JUN-2001; 2001US-0301889P.

(BURN-) BURNHAM INST.

XX

XX

XX

XX

XX

XX

Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
 Steiner-Liwen F;
 WPI; 2002-500222/53.
 P-PSDB; AAB24859.
 New polypeptide comprising a death domain or death effector domain,
 useful for discovery of drugs that suppress infection, inflammation,
 allergy, sepsis, autoimmunity, allograft rejection and other diseases.
 Claim 19; Page 180-182; 209pp; English.

CC The invention relates to an isolated polypeptide comprising a death
 CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention
 CC is useful for identifying a binding agent, preferably a protein or a drug
 CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC
 CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or
 CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and
 CC detecting the association of the domain and the candidate binding agent,
 CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or
 CC chemical crosslinking, nuclear magnetic resonance (NMR), mass
 CC spectroscopy (MS) and FPA. The invention is useful for modulating the
 CC level of a cell process such as cell proliferation, cell adhesion, cell
 CC stress responses, responses to microbial infection and B cell
 CC immunoglobulin class switching, in particular apoptosis within a cell.
 CC Antibody specifically reactive with CTDD DD of C. trachomatis, C.
 CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the
 CC CTDD DD protein is useful for detecting a Chlamydia infection. The
 CC invention is useful for modulating the activity of oncogenic proteins,
 CC for treating a pathology caused by the oncogenic proteins and for
 CC treating bacterial infections by modulating the activity of bacterial
 CC proteins. The protein and antibody specific for it are useful for
 CC discovery of drugs that suppress infection, inflammation, allergy,
 CC sepsis, autoimmunity, allograft rejection and other diseases. The protein
 CC is useful for treating immune-based pathologies, pathologies associated
 CC with cell division, inflammatory diseases such as sepsis, fibrosis,
 CC arthritis, graft versus host disease. The invention is used in antisense
 CC therapy and gene therapy. The present sequence is human IRAK4 gene
 CC
 XX
 SQ Sequence 1383 BP; 463 A; 243 C; 283 G; 394 T; 0 U; 0 Other;

Query Match 100.0%; Score 294; DB 6; Length 1383;
 Best Local Similarity 100.0%; Pred. No. 2.3e-77;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGCGGCTGCTCAATGTTGACTAATTAGAGAGCTGTCAGATTATTTATGATCT 60
 DB 25 ACAATATGCGGCTGCTCAATGTTGACTAATTAGAGAGCTGTCAGATTATTTATGATCT 84
 QY 61 CAAGAGAGATGAGAGAGTGTAGCTGTATTTAAATCAATCTGGTATGATATGATAC 120
 DB 85 CAGAGAGATGAGAGAGTGTAGCTGTATTTAAATCAATCTGGTATGATATGATAC 144
 QY 121 AATCAGTTTACATTAAGAGATTGGAAGCTTACTCAAACTGGAAGAGTCCACCTTC 180
 DB 145 AATCAGTTTACATTAAGAGATTGGAAGCTTACTCAAACTGGAAGAGTCCACCTTC 204
 QY 181 GAATTAATGTTGATGCTGGGCGACCAAAATTTGCAAGTTGATCTTGATCTTTTG 240
 DB 205 GAATTAATGTTGATGCTGGGCGACCAAAATTTGCAAGTTGATCTTGATCTTTTG 264
 QY 241 ATCCAAATGAAATTTTCTGCTCGGAGCTTTTGTCTCCAGATGCTGTTCC 294
 DB 265 ATCCAAATGAAATTTTCTGCTCGGAGCTTTTGTCTCCAGATGCTGTTCC 318

RESULT 5
 AAD59061
 ID AAD59061 standard; cDNA; 1383 BP.

AC AAD59061;

DT 18-DEC-2003 (first entry)

XX Human IRAK4 full length gene #1.

XX Human; death Domain; DD; death effector domain; DED; cell proliferation;
 KW Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
 KW neural growth factor receptor-interacting death domain; cell adhesion;
 KW vasculopathy; microbial infection; inflammation; allograft rejection; CTDD;
 KW cell stress responses; benign prostatic hyper trophy; antibacterial; NIDD;
 KW apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
 KW neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;
 KW keloid; interleukin-1 receptor-associated kinase; IRAK; gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 1..1383
 FT /*tag= a
 FT /product= "Human IRAK4 protein"

US2003049702-A1.

13-MAR-2003.

15-NOV-2001; 2001US-00001254.

17-NOV-2000; 2000US-00715893.

17-NOV-2000; 2000US-0367360P.

29-JUN-2001; 2001US-0301889P.

(REED/) REED J C.

(GODZ/) GODZIK A.

(PAML/) PAWLOWSKI K.

(FIOR/) FIORENTINO L.

(LEES/) LEE S H.

(ROTH/) ROTH W.

(STEN/) STENNER-LIEWEN F.

Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;

Stenner-Liewen F;

WPI; 2002-500222/53.

P-PSDB; AAB38902.

Claim 19; Fig 10A, 99p; English.

The present invention provides novel death Domain (DD) and death effector
 CC domain (DED) proteins and nucleic acids encoding them. The invention also
 CC provides death domain containing protein such as Chlamydia trachomatis
 CC death domain containing protein (CTDD) DD and neural growth factor
 CC receptor-interacting death domain (NIDD) DD. The invention is useful for
 CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED
 CC or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate
 CC binding agent and identifying an effective agent (e.g. protein or drug)
 CC that modulates the association of a DD, DED or NB-ARC domain with protein
 CC that binds the DD, DED or NB-ARC domain. The invention is also useful for
 CC modulating the level of cell process such as apoptosis, cell adhesion,
 CC cell proliferation, cell stress responses, responses to microbial
 CC infection and B cell immunoglobulin class switching. DEDs and NB-ARC
 CC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are
 CC useful for discovery of drugs that suppress infection, autoimmunity,
 CC inflammation, allergy, allograft rejection, sepsis and other diseases.
 CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy,
 CC autoimmunity, inflammation, allograft rejection, sepsis, keratinocytes
 CC hyperplasia, neoplasia, keloid, benign prostatic hyper trophy, fibrosis,
 CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries
 CC following balloon angioplasty (restenosis). The invention is also used in
 CC antibody therapy and gene therapy. The present sequence is human
 CC interleukin-1 receptor-associated kinase (IRAK)-4 full length gene
 CC
 XX
 SQ Sequence 1383 BP; 463 A; 243 C; 283 G; 394 T; 0 U; 0 Other;

Query Match 100.0%; Score 294; DB 6; Length 1383;
 Best Local Similarity 100.0%; Pred. No. 2.3e-77;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGCGGCTGCTCAATGTTGACTAATTAGAGAGCTGTCAGATTATTTATGATCT 60
 DB 25 ACAATATGCGGCTGCTCAATGTTGACTAATTAGAGAGCTGTCAGATTATTTATGATCT 84
 QY 61 CAAGAGAGATGAGAGAGTGTAGCTGTATTTAAATCAATCTGGTATGATATGATAC 120

Db 85 CAAAGAGATGAGAGAGATTGCTGTAGCTATTAAAAAACCTGTGATGATAGATAC 144
 Qy 121 AATCAGTTTCACATAGAGAGATTGAGCATTTACTTCAACTGAAAAAGTCCACTTCT 180
 Db 145 AATAGTTTCACATAGAGAGATTGAGCATTTACTTCAACTGAAAAAGTCCACTTCT 204
 Qy 181 GAATTACTGTTTGACTGGGGACCAACAATTGACAGTGTGTGATCTTTGGATCTTTTG 240
 Db 205 GAATTACTGTTTGACTGGGGACCAACAATTGACAGTGTGTGATCTTTGGATCTTTTG 264
 Qy 241 ATCCAAATGAAATTTTGTCTCTCGAGTCTTTTGTCTCCAGATGCTGTTCCC 294
 Db 265 ATCCAAATGAAATTTTGTCTCTCGAGTCTTTTGTCTCCAGATGCTGTTCCC 318
 RESULT 6
 AAS76805 standard; cDNA; 1668 BP.
 XX AAS76805;
 AC AAS76805;
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #12609.
 XX
 KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR P-PSDB; ABG12618.
 PT
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 PT
 PS Claim 1; SEQ ID NO 12609; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1668 BP; 571 A; 289 C; 332 G; 476 T; 0 U; 0 Other;
 XX
 Query Match 100.0%; Score 294; DB 5; Length 1668;
 Best Local Similarity 100.0%; Pred. No. 2,4e-77;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ACATATGTGGGCGCCCTCAATGTTTGGACTAATTAGAGAGCTGTGATTTATGATCCT 60
 Db 25 ACATATGTGGGCGCCCTCAATGTTTGGACTAATTAGAGAGCTGTGATTTATGATCCT 84
 Qy 61 CAAAGAGATGAGAGAGATTGAGCTGTAGCTATTAAAAAACCTGTGATGATAGATAC 120
 Db 85 CAAAGAGATGAGAGAGATTGAGCTGTAGCTATTAAAAAACCTGTGATGATAGATAC 144
 Qy 121 AATCAGTTTCACATAGAGAGATTGAGCATTTACTTCAACTGAAAAAGTCCACTTCT 180
 Db 145 AATCAGTTTCACATAGAGAGATTGAGCATTTACTTCAACTGAAAAAGTCCACTTCT 204
 Qy 181 GAATTACTGTTTGACTGGGGACCAACAATTGACAGTGTGTGATCTTTGGATCTTTTG 240
 Db 205 GAATTACTGTTTGACTGGGGACCAACAATTGACAGTGTGTGATCTTTGGATCTTTTG 264
 Qy 241 ATCCAAATGAAATTTTGTCTCTCGAGTCTTTTGTCTCCAGATGCTGTTCCC 294
 Db 265 ATCCAAATGAAATTTTGTCTCTCGAGTCTTTTGTCTCCAGATGCTGTTCCC 318
 RESULT 7
 AAD40085
 ID AAD40085 standard; DNA; 2817 BP.
 XX
 AC AAD40085;
 XX
 DT 22-OCT-2002 (first entry)
 XX
 DE Human IRAK4 gene #2.
 XX
 KW Human; death domain; DD; death effector domain; DED; Chlamydia infection;
 KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;
 KW inflammation; allergy; autoimmunity; allograft rejection; cell division;
 KW immune-based pathology; fibrosis; arthritis; graft versus host disease;
 KW immunosuppressive; gene therapy; antisense therapy; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200240680-A2.
 PD 23-MAY-2002.
 XX
 PF 15-NOV-2001; 2001WO-US044844.
 XX
 PR 17-NOV-2000; 2000US-00715893.
 PR 29-JUN-2001; 2001US-0301889P.
 XX
 PA (BURN-) BURNHAM INST.
 XX
 PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W,
 PI Steiner-Jewen F;
 XX
 DR WPI: 2002-500222/53.
 DR P-PSDB; AAE24865.
 XX
 CC New polypeptide comprising a death domain or death effector domain,
 CC useful for discovery of drugs that suppress infection, inflammation,
 CC allergy, sepsis, autoimmunity, allograft rejection and other diseases.

PS Claim 19; Page 194-196; 2099p; English.

XX The invention relates to an isolated polypeptide comprising a death
CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention
CC is useful for identifying a binding agent, preferably a protein or a drug
CC that binds a DD, DED or NB-ARC domain, by contacting a protein or a drug
CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or
CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and
CC detecting the association of the domain and the candidate binding agent, and
CC by yeast two hybrid assay, immunoprecipitation, SPR, ultraviolet (UV) or
CC chemical crosslinking, nuclear magnetic resonance (NMR), mass
CC spectroscopy (MS) and FPA. The invention is useful for modulating the
CC level of a cell process such as cell proliferation, cell adhesion, cell
CC stress responses, responses to microbial infection and B cell
CC immunoglobulin class switching, in particular apoptosis within a cell.
CC Antibody specifically reactive with CTDD DD of C. trachomatis, C.
CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the
CC CTDD DD protein is useful for detecting a Chlamydia infection. The
CC invention is useful for modulating the activity of oncogenic proteins,
CC for treating a pathology caused by the oncogenic proteins and for
CC treating bacterial infections by modulating the activity of bacterial
CC proteins. The protein and antibody specific for it are useful for
CC discovery of drugs that suppress infection, inflammation, allergy,
CC sepsis, autoimmunity, allograft rejection and other diseases. The protein
CC is useful for treating immune-based pathologies, pathologies associated
CC with cell division, inflammatory diseases such as sepsis, fibrosis,
CC arthritis, graft versus host disease. The invention is used in antisense
CC therapy and gene therapy. The present sequence is human IRAK4 gene
XX

SQ Sequence 2817 BP; 912 A; 547 C; 586 G; 772 T; 0 U; 0 Other;

Query Match 100.0%; Score 294; DB 6; Length 2817;
Best Local Similarity 100.0%; Pred. No. 2.9e-77;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGTGGCGCTGCTCAATGTGGACTAATAGGAAGCTGCAGATTTATGATCCT 60
Db 74 ACATATGTGGCGCTGCTCAATGTGGACTAATAGGAAGCTGCAGATTTATGATCCT 133

QY 61 CAAGAGATGTGAAGAGTTAGCTGTATTTAAACCATCTGGTATGATAGATAC 120
Db 134 CAAGAGAGATGTGAAGAGTTAGCTGTATTTAAACCATCTGGTATGATAGATAC 193

QY 121 AATCAGTTTACATTAAGAGATTTGAAGATTTCTTCAAACTGGAAAAAGTCCACTTCT 180
Db 194 AATCAGTTTACATTAAGAGATTTGAAGATTTCTTCAAACTGGAAAAAGTCCACTTCT 253

QY 181 GAATTAAGTGTGGAGTGGGACACCAAAATGGACAGTGGATCTTGTGATCTTTG 240
Db 254 GAATTAAGTGTGGAGTGGGACACCAAAATGGACAGTGGATCTTGTGATCTTTG 313

QY 241 ATCCAAATGAATTTTGTCTCTGAGATCTTTTCTCCAGATCTGTTCC 294
Db 314 ATCCAAATGAATTTTGTCTCTGAGATCTTTTCTCCAGATCTGTTCC 367

RESULT 8
AADS9067
ID AADS9067 standard; cDNA; 2817 BP.
XX
AC AADS9067;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human IRAK4 full length gene #2.
XX

KW Human; death Domain; DD; death effector domain; DED; cell proliferation;
KW Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
KW neuronal growth factor receptor-interacting death domain; cell adhesion;
KW vasotrophic; microbial infection; inflammation; allograft rejection; CTDD;
KW cell stress response; benign prostatic hypertrophy; antidiabetic; NIDD;
KW apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
KW neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;

KW keloid; interleukin-1 receptor-associated kinase; IRAK; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1432
FT /tag=a
FT /product="Human IRAK4 protein"
XX
XX US2003049702-A1.
XX
XX 13-MAR-2003.
XX
PF 15-NOV-2001; 2001US-00001254.
XX
PR 17-NOV-2000; 2000US-00715893.
PR 17-NOV-2000; 2000US-0367360P.
PR 29-JUN-2001; 2001US-0301889P.
XX
XX (REED/) REED J C.
PA (GODZ/) GODZIK A.
PA (PAWL/) PAWLOWSKI K.
PA (FIOR/) FIORENTINO L.
PA (LEES/) LEE S H.
PA (ROTH/) ROTH W.
PA (STEN/) STENNER-LIEWEN F.
XX
PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W,
PI Stenner-Liewen F;
XX
XX WPI; 2002-500222/53.
XX P-PSDB; AAE38908.
XX
XX New Polypeptide comprising a death domain or death effector domain,
XX useful for discovery of drugs that suppress infection, inflammation,
XX allergy, sepsis, autoimmunity, allograft rejection and other diseases.
XX
XX Claim 18; Page 51-53; 999p; English.

CC The present invention provides novel death Domain (DD) and death effector
CC domain (DED) proteins and nucleic acids encoding them. The invention also
CC provides death domain containing protein such as Chlamydia trachomatis
CC death domain containing protein (CTDD) DD and neural growth factor
CC receptor-interacting death domain (NIDD) DD. The invention is useful for
CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED
CC or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate
CC binding agent and identifying an effective agent (e.g. protein or drug)
CC that modulates the association of a DD, DED or NB-ARC domain with protein
CC that binds the DD, DED or NB-ARC domain. The invention is also useful for
CC modulating the level of cell process such as apoptosis, cell adhesion,
CC cell proliferation, cell stress responses, responses to microbial
CC infection and B cell immunoglobulin class switching. DEDs and NB-ARC
CC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are
CC useful for discovery of drugs that suppress infection, autoimmunity,
CC inflammation, allergy, allograft rejection, sepsis and other diseases.
CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy,
CC autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte
CC hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,
CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries
CC following balloon angioplasty (restenosis). The invention is also used in
CC antibody therapy and gene therapy. The present sequence is human
CC interleukin-1 receptor-associated kinase (IRAK)-4 full length gene
XX

SQ Sequence 2817 BP; 912 A; 547 C; 586 G; 772 T; 0 U; 0 Other;

Query Match 100.0%; Score 294; DB 6; Length 2817;
Best Local Similarity 100.0%; Pred. No. 2.9e-77;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGTGGCGCTGCTCAATGTGGACTAATAGGAAGCTGCAGATTTATGATCCT 60
Db 74 ACATATGTGGCGCTGCTCAATGTGGACTAATAGGAAGCTGCAGATTTATGATCCT 133

CC (GenBank accession number NM_016123)
 XX Sequence 2817 BP; 912 A; 547 C; 586 G; 772 T; 0 U; 0 Other;
 SQ

Query Match 100.0%; Score 294; DB 10; Length 2817;
 Best Local Similarity 100.0%; Pred. No. 2.3e-77;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGAGCCCTGCTCAATGTTGGACCTAATTTGGAAGCTGTGAGATTTATGATCCT 60
 DB 74 ACATATGAGCCCTGCTCAATGTTGGACCTAATTTGGAAGCTGTGAGATTTATGATCCT 133

QY 61 CAAGAGAGATGGAAGAAATTAGCTGTAGCTATTAAAAACCATCTGTGTGATGATATAC 120
 DB 134 CAAGAGAGATGGAAGAAATTAGCTGTAGCTATTAAAAACCATCTGTGTGATGATATAC 193

QY 121 AATCAGTTTCACATTAAGAGATTGAGATTCTTCAAACTGGAAAAAGTCCACTTCT 180
 DB 194 AATCAGTTTCACATTAAGAGATTGAGATTCTTCAAACTGGAAAAAGTCCACTTCT 253

QY 181 GAATTACTGTTGACTGGGGGACCAAAATTGSCAGATTGGATCTTGTGATCTTTTG 240
 DB 254 GAATTACTGTTGACTGGGGGACCAAAATTGSCAGATTGGATCTTGTGATCTTTTG 313

QY 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCCC 294
 DB 314 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCCC 367

RESULT 9
 ID ACC47548 standard; DNA; 2817 BP.
 XX ACC47548;
 AC ACC47548;
 XX
 DT 11-JUL-2003 (first entry)
 XX
 DE Human IL-1 receptor-associated kinase-4 sequence # SEQ ID 3.
 XX
 KW Antisense therapy; cytostatic; antimicrobial; antiinflammatory;
 KW interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer;
 KW inflammatory disease; infection; diagnostic; therapeutic; prophylaxis;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 50..1432
 FT /*tag= a
 FT /product= "IL-1 receptor-associated kinase-4"
 XX
 DE WO2003028636-A2.
 XX
 PD 10-APR-2003.
 XX
 PE 26-SEP-2002; 2002WO-US030574.
 XX
 PR 28-SEP-2001; 2001US-00966451.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett FC, Freiler SM;
 XX
 DR WPI; 2003-363256/34.
 DR P-PsDB; ABR44401.
 XX
 PT New antisense oligonucleotides for modulating IL-1 receptor-associated
 PT kinase-4 gene expression, particularly useful for preventing, delaying or
 PT treating e.g. cancer (e.g. renal cancer), inflammatory disease or an
 PT infection.
 XX
 PS Example 13; Page 80-83; 119pp; English.
 XX
 CC The invention relates to a compound of 8-50 nucleobases which is targeted
 CC to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated
 CC kinase-4, specifically hybridizing with the nucleic acid and inhibiting
 CC the expression of the encoded product. Also disclosed is the compound
 CC hybridizing with an 8-nucleobase portion of an active site on a nucleic
 CC acid molecule encoding IL-1 receptor-associated kinase-4. The antisense
 CC oligonucleotide is useful for treating an animal having a disease or
 CC conditions associated with IL-1 receptor-associated kinase-4, e.g. cancer
 CC (particularly renal cancer), inflammatory disease or an infection. The
 CC antisense compounds are useful for diagnostics, therapeutics,
 CC prophylaxis, or as research reagents or kits. The current sequence
 CC represents the human IL-1 receptor-associated kinase-4 encoding sequence

CC (GenBank accession number NM_016123)
 XX Sequence 2817 BP; 912 A; 547 C; 586 G; 772 T; 0 U; 0 Other;
 SQ

Query Match 100.0%; Score 294; DB 10; Length 2817;
 Best Local Similarity 100.0%; Pred. No. 2.3e-77;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATATGAGCCCTGCTCAATGTTGGACCTAATTTGGAAGCTGTGAGATTTATGATCCT 60
 DB 74 ACATATGAGCCCTGCTCAATGTTGGACCTAATTTGGAAGCTGTGAGATTTATGATCCT 133

QY 61 CAAGAGAGATGGAAGAAATTAGCTGTAGCTATTAAAAACCATCTGTGTGATGATATAC 120
 DB 134 CAAGAGAGATGGAAGAAATTAGCTGTAGCTATTAAAAACCATCTGTGTGATGATATAC 193

QY 121 AATCAGTTTCACATTAAGAGATTGAGATTCTTCAAACTGGAAAAAGTCCACTTCT 180
 DB 194 AATCAGTTTCACATTAAGAGATTGAGATTCTTCAAACTGGAAAAAGTCCACTTCT 253

QY 181 GAATTACTGTTGACTGGGGGACCAAAATTGSCAGATTGGATCTTGTGATCTTTTG 240
 DB 254 GAATTACTGTTGACTGGGGGACCAAAATTGSCAGATTGGATCTTGTGATCTTTTG 313

QY 241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCCC 294
 DB 314 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCCC 367

RESULT 10
 ID AAD10197 standard; cDNA; 1383 BP.
 XX AAD10197;
 AC AAD10197;
 XX
 DT 24-SEP-2001 (first entry)
 XX
 DE Human interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 cDNA.
 XX
 KW Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytostatic;
 KW IL; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD;
 KW chronic obstructive pulmonary disease; neuroprotective; chronic cough;
 KW adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS;
 KW interstitial lung disease; allergic rhinitis; transplant rejection;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke;
 KW cardiovascular disease; atherosclerosis; neurodegenerative disease;
 KW sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis;
 KW inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis;
 KW Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor;
 KW sarcoidosis; transgenic animal; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1383
 FT /*tag= a
 FT /product= "Human IRAK-4"
 XX
 DE WO200151641-A1.
 XX
 PD 19-JUL-2001.
 XX
 PR 12-JAN-2001; 2001WO-US001171.
 XX
 PR 13-JAN-2000; 2000US-0176395P.
 XX
 PA (TUDA-) TUDARIX INC.
 XX
 PI Wesche H, Li S;
 XX
 DR WPI; 2001-451860/48.
 DR P-PsDB; AAB05398.

XX Novel human interleukin-1 receptor associated kinase polypeptide, useful
PT for identifying modulators of the polypeptide for treating gout, asthma,
PT allergic rhinitis, multiple sclerosis and skin cancer.
PT
XX

PS Claim 7; Fig 2; 89pp; English.

The protein sequence is a cDNA encoding human interleukin (IL)-1 receptor associated kinase (IRAK)-4. IRAK associate with activated IL-1, IL-18 and other receptors and act to transduce signals originating from the activated receptors, ultimately leading to a variety of downstream effects such as nuclear factor (NF)- κ B activation. The IRAK-4 inhibitors are useful for treating inflammatory diseases such as pulmonary diseases and diseases of the airway (e.g., adult respiratory disease syndrome (ARDS), chronic obstructive pulmonary disease (COPD), pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or allergic rhinitis), transplant rejection, autoimmune diseases (e.g., rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or diabetes), cancer (e.g., solid tumour, skin cancer or lymphoma), cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of the central nervous system (e.g., neurodegenerative disease), CD14 mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis, psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic dermatitis), inflammatory bowel disease (e.g., Crohn's disease and ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout, sarcoidosis and ophthalmic diseases and conditions. The inhibitors of IRAK-4 activity or expression are used to inhibit signal transduction resulting from the activation of an interleukin-1 receptor (IL-1R)/Toll receptor in a cell. They also inhibit the activation of a transcription factor that activates NF κ B in the cell. IRAK-4 is used to create a nonhuman transgenic animal which is useful for testing the function of IRAK-4 in vivo, to generate models for the study of inflammatory disorders and conditions and for the development of potential treatments for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences are also used in gene therapy and in antisense therapy.

SQ Sequence 1383 BP; 463 A; 244 C; 283 G; 393 T; 0 U; 0 Other;

Query Match	99.5%	Score 292.4	DB 5	Length 1383
Best Local Similarity	99.7%	Pred. No. 6.9e-77		
Matches 293; Conservative	0	Mismatches 1	Indels 0	Gaps 0

QY 1 AACTATGTCGGCTGCTCAATGTTTGGACCTAATTAGGAAGCTGTCAGATTTTATGTATCCT 60

Db 25 AATATATGTCGGCTGCTCAATGTTTGGACCTAATTAGGAAGCTGTCAGATTTTATGTATCCT 84

QY 61 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTAAAAAACCACTGGTGAATGATAGTAC 120

Db 85 CAAGAAGATGGAAGAAGTTAGCTGTAGCTATTAAAAAACCACTGGTGAATGATAGTAC 144

QY 121 AATCGTTTCACATAAGGAGATTGGAAGCATTTACTTAAACCTGAAAAAAGTCCCACTTCT 180

Db 145 AATCGTTTCACATAAGGAGATTGGAAGCATTTACTTAAACCTGAAAAAAGTCCCACTTCT 204

QY 181 GAATTACTGTTGACTGGGGCACCAAAATGACAGTTGGTATCTGTGGATCTTTTG 240

Db 205 GAATTACTGTTGACTGGGGCACCAAAATGACAGTTGGTATCTGTGGATCTTTTG 264

QY 241 ATCCAAAATGAATTTTGTCTCTCTGCGAGCTTTTGTCTCCAGATCTGTTCCT 294

Db 265 ATCCAAAATGAATTTTGTCTCTCTGCGAGCTTTTGTCTCCAGATCTGTTCCT 318

```

RESULT 11
AAS61608
ID AAS61608 standard; cDNA; 501 BP.
vv

```

AC AAS61608;

DT 29-JAN-2002 (first entry)

Lung small cell carcinoma antigen, cDNA #149.

KM	Human; cytosolic; antitumour; lung small cell cancer antigen; tumour
KM	lung cancer; ss.
XX	
OS	
XX	Homo sapiens.
XX	
PN	WC200177168-A2.

PD 18-OCT-2001.

PF 11-APR-2001; 2001WO-US011859.

PR 11-APR-2000; 2000US-0196780P.

PR 01-SEP-2000; 2000US-0229763P.
DE 05 SEP 2000 0000Z
DD 05 SEP 2000 0000Z

PR 14-SEP-2000; 2000US-0232565P.
PR 19-DEC-2000; 2000US-0232565P.

PR 08-JAN-2001; 2001US-0260796P.
XX

PA (CORI-) CORIXA CORP.
XX

Pl Lodges MJ, wang T, Mohamath
XX

WFL; 2002-010896/01.

PT Lung tumor polynucleotide and diagnosis of cancer special11

PS Claim 1; Page 174: 295pp: End

CC The invention relates to novel

CC polynucleotides (1) and polyp
CC cancer in a patient. The meth

Sequence 501 BP; 166 A; 102 C; 97 G; 134 T; 0 U; 2 Other;

Sequence 501 BP; 166 A; 102 C; 97 G; 134 T; 0 U; 2 Other;

Query Match	82.2%;	Score 241.6;	DB 6;	Length 501;
Best Local Similarity	97.3%;	Pred. No. 7e-62;		
Matches 288; Conservative	0;	Mismatches 4;	Indels 4;	Gaps 4;

DQ Y I ACATGTGGCGCTGCCTCAATGTTGAATAATTAGACGCTCAGATTTTATTGACTCT 60
|||
DQ B 45 ACATGTGGCGCTGCCTCAATGTTGAATAATTAGACGCTCAGATTTTATTGACTCT 100

QY 61 CAAAGAGATGGAAGATTAGCTGTAGCTATTAAAAACCATCTGATGATAGATAC 12
Db 105 CAAAGAGATGGAAGATTAGCTGTAGCTATTAAAAACCATCTGATGATAGATAC 16

QY 121 AATC-AGTTTCACATAAGAATTGGAAGCATTACTTCAACTGAAAAAGTCCCACTTC 17
 |||||
Db 165 AATCAAGTTTCACATAAGAATTGGAAGCATTT-CTTCAAACGTGAAAAAAGTCCCACTTC 22

180 TGAATTACTGTTTGA CT- GGGGCAACCAAA TTGCA CAGTTGATCTTTGTGATCTTT 23
224 TTGATACTGTTTGA CTGGGGGCAACCAAA TTGCA CAGTTGATCTTTGTGATCTTT 28

239 TGATCCAAATGAAATTTTGGCTCTGCGATCTTTGGCCAGATGCTTCCC 294
284 TGATCCAAATGAAATTTTGGCTCTGCGATCTTTGGCCAGATGCTTCCC 338

RESULT 12
 AAD10198
 ID AAD10198 standard; cDNA, 1542 BP.
 AC AAD10198;
 XX
 XX
 DT 24-SEP-2001 (first entry)
 XX
 DE Mouse interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 cDNA.
 XX
 XX Mouse; interleukin-1 receptor associated kinase-4; IRAK-4; cytosolic;
 XX IL; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD;
 KW chronic obstructive pulmonary disease; neuroprotective; chronic cough;
 KW adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS;
 KW interstitial lung disease; allergic rhinitis; transplant rejection;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke;
 KW cardiovascular disease; atherosclerosis; neurodegenerative disease;
 KW sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis;
 KW inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis;
 KW Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor;
 KW sarcoidosis; transgenic animal; ss.
 XX
 XX Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1542
 FT /*tag= a
 FT /product= "Mouse IRAK-4"
 XX
 XX WO200151641-A1.
 XX
 PD 19-JUL-2001.
 XX
 PD 12-JAN-2001; 2001WO-US001171.
 XX
 PF 13-JAN-2000; 2000US-0176395P.
 XX
 PR (TULIA-) TULARIX INC.
 XX
 PA Weesche H, Li S;
 PI
 XX MPI: 2001-451860/48.
 DR P-PSDB; AAB05399.
 XX
 PT Novel human interleukin-1 receptor associated kinase polypeptide, useful
 PT for identifying modulators of the polypeptide for treating gout, asthma,
 PT allergic rhinitis, multiple sclerosis and skin cancer.
 XX
 PS Claim 26; Fig 4; 89pp; English.
 XX
 XX The present sequence is a cDNA encoding mouse interleukin (IL)-1 receptor
 CC associated kinase (IRAK)-4. IRAK associate with activated IL-1, IL-18 and
 CC other receptors and act to transduce signals originating from the
 CC activated receptors, ultimately leading to a variety of downstream
 CC effects such as nuclear factor (NF)-kappaB activation. The IRAK-4
 CC inhibitors are useful for treating inflammatory diseases such as
 CC pulmonary diseases and diseases of the airway (e.g., adult respiratory
 CC disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD),
 CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or
 CC allergic rhinitis), transplant rejection, autoimmune diseases (e.g.,
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or
 CC diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma),
 CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of
 CC the central nervous system (e.g., neurodegenerative disease), CD14
 CC mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis,
 CC psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic
 CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and
 CC ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout,
 CC sarcoidosis and ophthalmic diseases and conditions. The inhibitors of
 CC IRAK-4 activity or expression are used to inhibit signal transduction

CC resulting from the activation of an interleukin-1 receptor (IL-1R)/Toll
 CC receptor in a cell. They also inhibit the activation of a transcription
 CC factor that activates NFkappaB in the cell. IRAK-4 is used to create a
 CC nonhuman transgenic animal which is useful for testing the function of
 CC IRAK-4 in vivo, to generate models for the study of inflammatory
 CC disorders and conditions and for the development of potential treatments
 CC for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences
 CC are also used in gene therapy and in antisense therapy
 XX
 SQ Sequence 1542 BP; 421 A; 392 C; 423 G; 306 T; 0 U; 0 Other;
 Query Match 69.5%; Score 204.4; DB 5; Length 1542;
 Best Local Similarity 81.0%; Pred. No. 1.3e-50;
 Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
 QY 1 ACATATGCGCGCTGCTCAATGTTGACTAATTAGAGAGCTGCAGATTATGATCTT 60
 DB 187 ACATACATACCGAACCTTAATGTTGGGATCCTTTAGGAAGCTGTGGATTATGATCTT 246
 QY 61 CAAGAAGGATGGAAGATTAGTCTAGCTATTAAACCATCTGCGATGATATAC 120
 DB 247 CAAGAAGGATGGAAGATTAGTCTAGCTATTCAAAAAGCGTCCGGGACAGAGATAC 306
 QY 121 AATCAGTTTCAATPAGAGATTGTAAGCATTTACTTCAAACTGAAAAAGTCCACTTCT 180
 DB 307 AATCAGTTTCAATPAGAGATTGTAAGCATTTACTTCAAGCTTACTTCAAGCGGAGAGCCCACTGT 366
 QY 181 GAATTCATCTTTGACTGGGGCAACCAATTCACAGTTGATCTTGTGATCTTTTG 240
 DB 367 GAATTCATCTTTGACTGGGGCAACCAATTCACAGTTGATCTTGTGATCTTTTG 426
 QY 241 ATCCAAATGAAATTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTCC 294
 DB 427 GTCCAGATTGAGCTGTTCCTCCCGCCACTCTCTCTGCGGATGCCGTTCC 480
 RESULT 13
 ACC47549
 ID ACC47549 standard; DNA, 31000 BP.
 XX
 AC ACC47549;
 XX
 DT 11-JUL-2003 (first entry)
 XX
 DE Human DNA complement sequence # SBQ ID 10.
 XX
 KW Antisense therapy; cytosolic; antimicrobial; antiinflammatory;
 KW interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer;
 KW inflammatory disease; infection; diagnostic; therapeutic; prophylaxis;
 KW ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003028636-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 26-SEP-2002; 2002WO-US030574.
 XX
 PR 28-SEP-2001; 2001US-00966451.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett FC, Freier SM;
 XX MPI: 2003-363256/34.
 DR
 XX
 PT New antisense oligonucleotides for modulating IL-1 receptor-associated
 PT kinase-4 gene expression, particularly useful for preventing, delaying or
 PT treating e.g. cancer (e.g. renal cancer), inflammatory disease or an
 PT infection.
 XX
 PS Example 15; Page 85-102; 119pp; English.

XX The invention relates to a compound of 8-50 nucleobases which is targeted
 CC to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated
 CC kinase-4, specifically hybridising with the nucleic acid and inhibiting
 CC the expression of the encoded product. Also disclosed is the compound
 CC hybridising with an 8-nucleobase portion of an active site on a nucleic
 CC acid molecule encoding IL-1 receptor-associated kinase-4. The antisense
 CC oligonucleotide is useful for treating an animal having a disease or
 CC (particularly renal cancer), inflammatory disease or an infection. The
 CC antisense compounds are useful for diagnostics, therapeutics,
 CC prophylaxis, or as research reagents or kits. The current sequence is
 CC utilised in an example from the invention in the design of antisense
 CC oligonucleotides, and represents the complement of the human DNA sequence
 CC that is given as GenBank accession number AC016143
 XX

SQ Sequence 31000 BP; 9247 A; 5856 C; 5924 G; 9973 T; 0 U; 0 Other;

Query Match 51.6%; Score 151.8; DB 10; Length 31000;
 Best Local Similarity 95.7%; Pred. No. 1.7e-34;
 Matches 156; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 123 TCACTTACATAGAGATTGAGCATTCTTCAACTGGAAAAAGTCCCACTTCTGA 182
 DB 12953 TTAATTACTTTTAAAGAGATTGAGCATTCTTCAACTGGAAAAAGTCCCACTTCTGA 13012
 QY 183 ATTACTGTTGACTGGGACACCAAAATTGACAGTTGGATCTTGTGATCTTTGAT 242
 DB 13013 ATTACTGTTGACTGGGACACCAAAATTGACAGTTGGATCTTGTGATCTTTGAT 13072
 QY 243 CCAAAATGAATTTTGTCTCTGAGTCTTTGTCTCCAGAT 285
 DB 13073 CCAAAATGAATTTTGTCTCTGAGTCTTTGTCTCCAGAT 13115

RESULT 14
 AAS76803
 ID AAS76803 standard; cDNA; 405 BP.

XX AAS76803;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #12607.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

OS WO200175067-A2.

PN 11-OCT-2001.

PD 30-MAR-2001; 2001WO-US008631.

PF 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HSE-) HSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

XX P-PSDB; ABG12616.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

PS Claim 1; SEQ ID NO 12607; 103bp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probe, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 405 BP; 93 A; 87 C; 83 G; 142 T; 0 U; 0 Other;

Query Match 51.2%; Score 150.4; DB 5; Length 405;
 Best Local Similarity 99.3%; Pred. No. 1e-34;
 Matches 151; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 134 TAAGGAGATTGAGCATTCTTCAACTGGAAAAAGTCCCACTTGTGATCTTTG 193
 DB 115 TAAGGAGATTGAGCATTCTTCAACTGGAAAAAGTCCCACTTGTGATCTTTG 174
 QY 194 ACTGGGGACACCAAAATTGACAGTTGGATCTTGTGATCTTTGATCTTTGAT 253
 DB 175 ACTGGGGACACCAAAATTGACAGTTGGATCTTGTGATCTTTGATCTTTGAT 234
 QY 254 TTTTGTCTCTGCGAGTCTTTGTCTCCAGAT 285
 DB 235 TTTTGTCTCTGCGAGTCTTTGTCTCCAGAT 266

RESULT 15
 AAD40084
 ID AAD40084 standard; DNA; 211 BP.

XX AAD40084;

DT 22-OCT-2002 (first entry)

DE Human IRAK4 short gene.

KW Human; death domain; DD; death effector domain; DED; Chlamydia infection;
 KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;
 KW inflammation; allergy; autoimmunity; allograft rejection; cell division;
 KW immune-based pathology; fibrosis; arthritis; graft versus host disease;
 KW immunosuppressive; gene therapy; antisense therapy; gene; ds.

XX Homo sapiens.

OS WO200240680-A2.

PN 23-MAY-2002.

PD 15-NOV-2001; 2001WO-US044844.

PF 17-NOV-2000; 2000US-00715893.

PR 29-JUN-2001; 2001US-0301889P.

XX Key Location/Qualifiers

FT CDS 1..180

FT /tag= a

FT /product= "Human IRAK4 short protein"

PA (BURN-) BURHAM INST.

XX Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W,
PI Steiner-Liwen F,

XX WPI; 2002-500222/53.
DR P-PSDB; AAE24864.

XX
PT New polypeptide comprising a death domain or death effector domain,
PT useful for discovery of drugs that suppress infection, inflammation,
PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.

XX
PS Claim 19; Page 195; 209pp; English.

XX
CC The invention relates to an isolated polypeptide comprising a death
CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention
CC is useful for identifying a binding agent, preferably a protein or a drug
CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC
CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or
CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and
CC detecting the association of the domain and the candidate binding agent,
CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or
CC chemical crosslinking, nuclear magnetic resonance (NMR), mass
CC spectroscopy (MS) and FPA. The invention is useful for modulating the
CC level of a cell process such as cell proliferation, cell adhesion, cell
CC stress responses, responses to microbial infection and B cell
CC immunoglobulin class switching, in particular apoptosis within a cell.
CC Antibody specifically reactive with CTDD DD of C. trachomatis, C.
CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the
CC CTDD DD protein is useful for detecting a Chlamydia infection. The
CC invention is useful for modulating the activity of oncogenic proteins,
CC for treating a pathology caused by the oncogenic proteins and for
CC treating bacterial infections by modulating the activity of bacterial
CC proteins. The protein and antibody specific for it are useful for
CC discovery of drugs that suppress infection, inflammation, allergy,
CC sepsis, autoimmunity, allograft rejection and other diseases. The protein
CC is useful for treating immune-based pathologies, pathologies associated
CC with cell division, inflammatory diseases such as sepsis, fibrosis,
CC arthritis, graft versus host disease. The invention is used in antisense
CC therapy and gene therapy. The present sequence is human IRAK4 short gene
XX
SQ Sequence 211 BP; 77 A; 41 C; 36 G; 57 T; 0 U; 0 Other;

Query Match 46.8%; Score 137.6; DB 6; Length 211;
Best Local Similarity 97.2%; Pred. No. 5.5e-31;
Matches 140; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 61 CAAGAAGATGGAAGAGTGTAGCTGATTTAAAAAACCATCTGTGTGATGATGATAC 120
DB 85 CAAGAAGATGGAAGAGTGTAGCTGATTTAAAAAACCATCTGTGTGATGATGATAC 144
QY 121 AATCAGTTTCATATAGAGATT 144
DB 145 AATCAGTTTCATATAGAGATT 168

Search completed: January 12, 2005, 04:35:56
Job time: 321 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 03:29:43 ; Search time 1843 Seconds
(without alignments)
7543.772 Million cell updates/sec

Title: US-10-001-254-5
Perfect score: 294
Sequence: 1 acatattgctgcgcctcctca.....tgcctccagatgctgtccc 294

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
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2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	294	100.0	294	AX431296	Sequence
2	294	100.0	833	AR223870	Sequence
3	294	100.0	1383	AX431306	Sequence
4	294	100.0	1636	AY340962	Homo sapi
5	294	100.0	1684	AY340963	Homo sapi
6	294	100.0	2775	CQ728380	Sequence
7	294	100.0	2817	AR475548	Sequence
8	294	100.0	2817	AX431318	Sequence
9	294	100.0	2817	AR155118	Homo sapi
10	294	100.0	2820	AK000528	Homo sapi
11	292.4	99.5	1383	AY283671	Homo sapi
12	292.4	99.5	1383	AY196260	Sequence
13	292.4	99.5	1383	AF445802	Homo sapi
14	292.4	99.5	1383	AY283670	Homo sapi
15	292.4	99.5	1629	BC013316	Homo sapi
16	241.6	82.2	501	AX321132	Sequence
17	217	73.8	1703	AY340966	Homo sapi
18	217	73.8	1751	AY340967	Homo sapi
19	204.4	69.5	1542	AX196262	Sequence

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21	204.4	69.5	2431	10	BC051676	BC051676 Mus muscu
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23	151.8	51.6	33033	9	AY186092	AY186092 Homo sapi
24	151.8	51.6	118572	2	AC093012	AC093012 Homo sapi
25	151.8	51.6	165868	2	AC021719	AC021719 Homo sapi
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36	94.8	32.2	1452	5	AV161584	AV161584 Danto rer
37	94.8	32.2	1719	5	BC045381	BC045381 Danto rer
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39	61.4	20.9	252400	2	AC094859	AC094859 Rattus no
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ALIGNMENTS

RESULT 1	AX431296	294 bp	DNA	linear	PAT 28-JUN-2002
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DEFINITION	AX431296				
ACCESSION	AX431296				
VERSION	AX431296.1	GI:21656165			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	1	Pawlowski, K., Fiorentino, L., Godzik, A., Lee, S. H., Reed, J. C.,			
AUTHORS	Roth, W. and Stenner-Ilewen, F.				
TITLE	Novel death domain proteins				
JOURNAL	Patent: WO 0240680-A 5 23-MAY-2002;				
BURNHAM	INST (US)				
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QY 121 AATCAGTTTCACATAAGAGAGATTGAAAGCATTTACTTAAACGTGAAAAAGTCCCACTTCT 180
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Query Match	100.0%;	Score 294;	DB 6;	Length 833;
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QY	121	AATCAGTTTCCATTAAGAGAGATTTTGAAGCATTTACTT	CAAACTGGAAGAAAAGTCCCACTTCT 180	
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TITLE
JOURNAL
AUTHOR
Koch, W. and Steimer-Liwen, F.
Novel death domain proteins
Patent: WO 0240680-A 15 23-MAY-2002;
BURNHAM
INST (US)
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QY	1 ACATATGTCGGCTGCCTCAATGTTTGA	CTAATTAGGAAGCTGTCA	GATTTTATGATCCT	60	
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Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CAAGAAGATGAAGAAGTTAGCTGTAGCTATTTAAAAACATCTGTGATGATGATAC 120
Db 150 CAAGAAGATGAAGAAGTTAGCTGTAGCTATTTAAAAACATCTGTGATGATGATAC 209
Qy 121 AATGAGTTTCACATPAGAGATTTGAAAGCAATTAATGAAAAAGTCCCACTTCT 180
Db 210 AATGAGTTTCACATPAGAGATTTGAAAGCAATTAATGAAAAAGTCCCACTTCT 269
Qy 181 GAATTAAGTTGAGCTGGGGACCAACAATTGACAGTGTGATCTTGGATCTTTTG 240
Db 270 GAATTAAGTTGAGCTGGGGACCAACAATTGACAGTGTGATCTTGGATCTTTTG 329
Qy 241 ATCCAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTTCCC 294
Db 330 ATCCAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTTCCC 383

RESULT 5 1684 bp mRNA linear PRI 01-AUG-2004
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LOCUS Homo sapiens interleukin-1 receptor-associated kinase 4 variant
DEFINITION (IRAK4) mRNA, complete cds, alternatively spliced.
ACCESSION AY340963
VERSION AY340963.1 GI:37727960
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1684)
AUTHORS Chuang,T.H. and Ulevitch,R.J.
TITLE Human interleukin-1 receptor associated kinase 4 cDNA sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1684)
AUTHORS Chuang,T.H. and Ulevitch,R.J.
TITLE Direct Submission
JOURNAL Submitted (14-JUL-2003) Immunology, The Scripps Research Institute,
10550 North Torrey Pines Rd., La Jolla, CA 92037, USA
location/Qualifiers

FEATURES

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Db 198 CAAGAAGATGAAGAAGTTAGCTGTAGCTATTTAAAAACATCTGTGATGATGATAC 257
Qy 121 AATGAGTTTCACATPAGAGATTTGAAAGCAATTAATGAAAAAGTCCCACTTCT 180
Db 258 AATGAGTTTCACATPAGAGATTTGAAAGCAATTAATGAAAAAGTCCCACTTCT 317
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Qy 241 ATCCAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTTCCC 294
Db 378 ATCCAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTTCCC 431

RESULT 6

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DEFINITION CQ728380
ACCESSION CQ728380
VERSION CQ728380.1 GI:42297030
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,B.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof

JOURNAL Patent: WO 02068579-A 14314 06-SEP-2002;
PB Corporation (NY) (US)
location/Qualifiers
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96 CAAGAAGATGGAAGAAGTTAGCTGTAATTTAAACCATCTGGTATGATAGATAC 155
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156 AATCAGTTTCACTAAGAGATTTGAGCATTTCTCAAACTGGAAGAAAGTCCACTTCT 215
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DEFINITION Sequence 3 from patent US 6692959.
ACCESSION AR475548
VERSION AR475548.1 GI:42715031
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2817)
AUTHORS Bennett,C.F. and Freier,S.M.
TITLE Antisense modulation of IL-1 receptor-associated kinase-4
JOURNAL Patent: US 6692959-A 3 17-FEB-2004;
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Db 314 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTGCTCCAGATGCTGTTCC 367

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DEFINITION Sequence 27 from Patent WO0240680.
ACCESSION AX431318
VERSION AX431318.1 GI:21656187
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Pawlowski,K., Fiorentino,L., Godzik,A., Lee,S.H., Reed,J.C., Roth,W. and Steiner-Hewen,F.
TITLE Novel death domain proteins
JOURNAL Patent: WO 0240680-A 27 23-MAY-2002;
BURNHAM INST (US)
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134 CAAGAAGATGGAAGAAGTTAGCTGTAATTTAAACCATCTGGTATGATAGATAC 193
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241 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTGCTCCAGATGCTGTTCC 294
314 ATCCAAATGAATTTTGTCTCTGCGAGTCTTTGCTCCAGATGCTGTTCC 367

RESULT 9
LOCUS AF155118 2817 bp mRNA linear PRI 05-JAN-2000
DEFINITION Homo sapiens putative protein kinase NY-BEN-64 antigen mRNA,
complete cds.
ACCESSION AF155118
VERSION AF155118.1 GI:5360130

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Scalan, M.J., Jordan, J.D., Williamson, B., Stockert, E., Bander, N.H., Jorgensen, V., Gure, A.O., Jager, D., Jager, E., Knuth, A., Chen, Y.-T., and Old, L.J.
TITLE Antigen recognized by autologous antibody in patients with renal-cell carcinoma
JOURNAL Int. J. Cancer 83 (4), 456-464 (1999)
MEDLINE 99438124
PUBMED 10508479
REFERENCE 2 (bases 1 to 2817)
AUTHORS Scalan, M.J., Jordan, J.D., Williamson, B., Stockert, E., Bander, N.H., Jorgensen, V., Gure, A.O., Jager, D., Jager, E., Knuth, A., Chen, Y.-T., and Old, L.J.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-1999) Ludwig Institute, Sloan-Kettering Institute, 1275 York Ave, New York, NY 10021, USA
FEATURES
SOURCE Location/Qualifiers
1..2817
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="1973/10-4"
/cell_type="renal cell carcinoma"
50..1432
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/db_xref="GI:5360131"
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ORIGIN
Query Match 100.0%; Score 294; DB 9; Length 2817;
Best Local Similarity 100.0%; Pred. No. 1.6e-64;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACATATGTCGCGCTCCCTCAATGTTGACTAATTAAGAGAGTGTGATTTATGATCCT 60
Db 74 ACATATGTCGCGCTCCCTCAATGTTGACTAATTAAGAGAGTGTGATTTATGATCCT 133
QY 61 CAAGAAGATGGAAGAGTTAGCTGTAGCTATTAAAAACCATCTGCTGATGATAGATAC 120
Db 134 CAAGAAGATGGAAGAGTTAGCTGTAGCTATTAAAAACCATCTGCTGATGATAGATAC 193
QY 121 AATGAGTTTCACATPAAGAGATTGAAGCATTAATCAATGAGAAAAAGTCCCATCTCT 180
Db 194 AATGAGTTTCACATPAAGAGATTGAAGCATTAATCAATGAGAAAAAGTCCCATCTCT 253
QY 181 GAATTAAGTTGTTGACTGGGGACCACAAAATGTCACAGTTGGTGAATCTTGATCTTTTG 240
Db 254 GAATTAAGTTGTTGACTGGGGACCACAAAATGTCACAGTTGGTGAATCTTTTG 313
QY 241 ATCCAAATGAATTTTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCC 294
Db 314 ATCCAAATGAATTTTTTGTCTCTGCGAGTCTTTTGTCTCCAGATGCTGTTCC 367

RESULT 10
AK000528 2820 bp mRNA linear PRI 13-SEP-2003
LOCUS
DEFINITION Homo sapiens cDNA FLJ20521 f18, clone KAT10395.

ACCESSION AK000528
VERSION AK000528.1 GI:7020683
KEYWORDS oligo capping; f18 (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Watanabe, K., Kumagai, A., Itakura, S., Yamazaki, M., Tashiro, H., Ota, T., Suzuki, Y., Okeyashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isega, T. and Sugano, S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 2820)
Sugano, S., Suzuki, Y., Ota, T., Okeyashi, M., Nishi, T., Isega, T., Shibahara, T., Tanaka, T. and Nakamura, Y.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Department of Virology; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: f18cna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing; Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).
FEATURES
SOURCE Location/Qualifiers
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/clone_id="KAT"
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ORIGIN
Query Match 100.0%; Score 294; DB 9; Length 2820;
Best Local Similarity 100.0%; Pred. No. 1.6e-64;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACATATGTCGCGCTCCCTCAATGTTGACTAATTAAGAGAGTGTGATTTATGATCCT 60
Db 54 ACATATGTCGCGCTCCCTCAATGTTGACTAATTAAGAGAGTGTGATTTATGATCCT 113
QY 61 CAAGAAGATGGAAGAGTTAGCTGTAGCTATTAAAAACCATCTGCTGATGATAGATAC 120
Db 114 CAAGAAGATGGAAGAGTTAGCTGTAGCTATTAAAAACCATCTGCTGATGATAGATAC 173
QY 121 AATGAGTTTCACATPAAGAGATTGAAGCATTAATCAATGAGAAAAAGTCCCATCTCT 180
Db 174 AATGAGTTTCACATPAAGAGATTGAAGCATTAATCAATGAGAAAAAGTCCCATCTCT 233
QY 181 GAATTAAGTTGTTGACTGGGGACCACAAAATGTCACAGTTGGTGAATCTTGATCTTTTG 240
Db 234 GAATTAAGTTGTTGACTGGGGACCACAAAATGTCACAGTTGGTGAATCTTTTG 293

Db 265 ATCCAAATGAATTTTGTCTCGCAGTCTTTGTCTCCAGATGCTGCC 318

RESULT 13
AP445802 1383 bp mRNA linear PRI 20-APR-2002
LOCUS Homo sapiens interleukin-1 receptor associated kinase 4 (IRAK4)
DEFINITION mRNA, complete cds.
ACCESSION AF445802.1 GI:20219009
VERSION AF445802.1 GI:20219009
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1383)
AUTHORS Li,S., Strejlow,A., Fontana,E.J. and Wesche,H.
TITLE IRAK-4: a novel member of the IRAK family with the properties of an IRAK-kinase
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (8), 5567-5572 (2002)
MEDLINE 21957277
PUBMED 11960013
REFERENCE 2 (bases 1 to 1383)
AUTHORS Suzuki,N., Suzuki,S., Duncan,G.S., Miliar,D.G., Wada,T.,
Martens,C., Takada,H., Wakeham,A., Itie,A., Li,S., Penninger,J.M.,
Wesche,H., Ohashi,P.S., Mak,T.W. and Yeh,W.C.
TITLE Severe impairment of interleukin-1 and Toll-like receptor signalling in mice lacking IRAK-4
JOURNAL Nature 416 (6882), 750-756 (2002)
MEDLINE 21959395
PUBMED 11923871
REFERENCE 3 (bases 1 to 1383)
AUTHORS Li,S., Strejlow,A., Fontana,E.J. and Wesche,H.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-2001) Biology I, Tularik Inc., 2 Corporate Drive,
South San Francisco, CA 94080, USA
FEATURES
source location/Qualifiers
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/mol_type="mRNA"
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VDITBELKQOPDOIKNVAKCOHENLVELLGFSSDGLCLVYVWPNGLDRISC
LDGTPPLSPWMRCKIAOGANGIFLPHNNHHRDITSAANTLDBATLAKISDGLAR
ASEKPAQVTMTSRIVGTITVAPALRGELTPSDIYSPGVVLEIITGLPAVDENRE
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QQLQLEWTAS"

ORIGIN
Query Match 99.5%; Score 292.4; DB 9; Length 1383;
Best Local Similarity 99.7%; Pred. No. 4.3e-64;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACATATGTGCGTCTGCTCAATGTGACTAATTAAGAAAGTGTGAGATTTATGATCCT 60
Db 25 ACATATGTGCGTCTGCTCAATGTGACTAATTAAGAAAGTGTGAGATTTATGATCCT 84
QY 61 CAAGAAGATGAGAAAGATTAGCTGTAGCTATTAAAAACCATGTGTGATGATAGATAC 120
Db 85 CAAGAAGATGAGAAAGATTAGCTGTAGCTATTAAAAACCATGTGTGATGATAGATAC 144

QY 121 AATCAGTTTCAATPAAGAGATTGAGCATTAATTCAAACTGGAAGAAAGTCCACTTCT 180
Db 145 AATCAGTTTCAATPAAGAGATTGAGCATTAATTCAAACTGGAAGAAAGTCCACTTCT 204
QY 181 GAATTACTGTTTGACTGGGACACCAAAATTCGACAGTGTGTATCTTTGGATCTTTTG 240
Db 205 GAATTACTGTTTGACTGGGACACCAAAATTCGACAGTGTGTATCTTTGGATCTTTTG 264
QY 241 ATCCAAATGAATTTTGTCTCTCGCAGTCTTTGTCTCCAGATGCTGCC 294
Db 265 ATCCAAATGAATTTTGTCTCTCGCAGTCTTTGTCTCCAGATGCTGCC 318

RESULT 14
AY283670 1383 bp mRNA linear PRI 17-JUN-2003
LOCUS Homo sapiens interleukin-1 receptor associated kinase 4 mutant form
DEFINITION 1 (IRAK4) mRNA, complete cds.
ACCESSION AY283670
VERSION AY283670.1 GI:31871817
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1383)
AUTHORS Medvedev,A.E., Lentschat,A., Kuhns,D.B., Blanco,J.C.G.,
Salkowski,C., Zhang,S., Arditi,M., Gallin,J.I. and Vogel,S.N.
TITLE Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to Lipopolysaccharide and Interleukin-1 in a Patient with Recurrent Bacterial Infections
JOURNAL J. Exp. Med. (2003) In press
REFERENCE 2 (bases 1 to 1383)
AUTHORS Medvedev,A.E., Lentschat,A., Kuhns,D.B., Blanco,J.C.G.,
Salkowski,C., Zhang,S., Arditi,M., Gallin,J.I. and Vogel,S.N.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2003) Microbiology and Immunology, University of Maryland, Baltimore, 655 West Baltimore Street, Baltimore, MD 21201-1559, USA
FEATURES
source location/Qualifiers
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/mol_type="mRNA"
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1..879
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/note="IRAK-4 mutated form 1; truncated protein kinase due to premature stop codon"
/codon_start=1
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DAVPTKNTLPSKALITVOOKPFCDKRTLTMTVPONLEQSTMPDSSPENSLELV
SDTRFHSFSEYELKNTNNFDERPISVGNNKMGEGGVVYKGVNNTTVAVKKLAM
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variation

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
231.286 Million cell updates/sec

Title: US-10-001-254-6
Perfect score: 517
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Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517	100.0	98	5	AAE24854 Human IRA
2	517	100.0	98	5	AAE38897 Human IRA
3	517	100.0	206	3	AAI92347 Human can
4	517	100.0	455	4	ABG12618 Novel hum
5	517	100.0	460	5	AAE24859 Human IRA
6	517	100.0	460	5	AAE24865 Human IRA
7	517	100.0	460	5	AAE38908 Human IRA
8	517	100.0	460	5	AAE38902 Human IRA
9	517	100.0	460	6	ABR44401 Human IL-
10	517	100.0	460	8	ADO44001 Amino aci
11	513	99.2	191	4	AAE05402 Truncated
12	513	99.2	460	4	AAE05398 Human int
13	513	99.2	460	4	AAE05401 Human IRA
14	513	99.2	460	4	AAE05403 Human IRA
15	507	98.1	460	4	AAE05404 Human IRA
16	476	92.1	459	4	AAE05399 Mouse int
17	473	91.5	459	4	AAE05405 Mouse IRA
18	473	91.5	459	4	AAE05406 Mouse IRA
19	256	49.5	102	4	ABG12616 Novel hum
20	247	47.8	59	5	AAE24864 Human IRA
21	247	47.8	59	5	AAE38907 Human IRA
22	247	47.8	60	8	ABE28317 Human KRP
23	245	47.4	127	4	ABG12615 Novel hum
24	96.5	18.7	596	3	AAI69406 A human i
25	96.5	18.7	596	4	AAE65667 Novel i

26	96.5	18.7	596	4	AAE48173 Interleuk
27	96.5	18.7	596	8	ADI29275 Human MAR
28	96.5	18.7	597	4	AAE48172 Interleuk
29	96.5	18.7	599	4	AAE38644 Human pol
30	96.5	18.7	622	4	ABG22715 Novel hum
31	95	18.4	609	7	ADB61346 Murine IR
32	84	16.2	497	2	ABG03007 Novel hum
33	79	15.3	590	2	AAE08653 Human IRA
34	79	15.3	590	7	ADE40441 Human IRA
35	79	15.3	625	2	AAE08654 Human IRA
36	77	14.9	251	6	AAE37948 Murine My
37	72.5	14.0	813	5	AAU97836 Human cys
38	72.5	14.0	824	3	AAE41026 Human ORF
39	72.5	14.0	824	5	ABE61489 Human NF-
40	72.5	14.0	824	5	AAU97838 Human cys
41	72.5	14.0	824	8	ADN04325 Antipsori
42	72.5	14.0	824	8	ADP82021 Human muc
43	72	13.9	462	4	ABE65115 Drosophi
44	71.5	13.8	5836	8	ADK16042 Streptomy
45	71	13.7	259	7	ADF30722 Rat angio

ALIGNMENTS

RESULT 1	AAE24854	AAE24854 standard; peptide: 98 AA.
XX	AC	AAE24854:
XX	XX	
DT	22-OCT-2002	(first entry)
XX	XX	
DE	Human IRA4 DD. (death domain) protein.	
XX	XX	
KW	Human; death domain; DD; death effector domain; DED; Chlamydia infection; NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy.	
KM	Homo sapiens.	
OS	XX	
XX	XX	WO200240680-A2.
PN	23-MAY-2002.	
PD	XX	
XX	XX	
PF	15-NOV-2001; 2001WO-US044844.	
XX	XX	
PR	17-NOV-2000; 2000US-00715893.	
FR	29-JUN-2001; 2001US-0301889P.	
PA	(BURN-) BURHAM INST.	
XX	XX	
PI	Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W; Stenmet-Liwen F;	
PI	WPI; 2002-500222/53.	
DR	N-PSDB; AAD40074.	
XX	XX	
PT	New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.	
PT	Claim 1; Page 174; 209pp; English.	
PS	XX	
CC	The invention relates to an isolated polypeptide comprising a death domain (DD), death effector domain (DED) or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a protein or a drug domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or NIDP (NGFR-interacting Death Domain), with a candidate binding agent and detecting the association of the domain and the candidate binding agent,	

by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or chemical crosslinking, nuclear magnetic resonance (NMR), mass spectroscopy (MS) and FPA. The invention is useful for modulating the level of a cell process such as cell proliferation, cell adhesion, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching, in particular apoptosis within a cell. Antibody specifically reactive with CTDD DD of C. trachomatis, C. muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the CTDD DD protein is useful for detecting a Chlamydia infection. The invention is useful for modulating the activity of oncogenic proteins, for treating a pathology caused by the oncogenic proteins and for treating bacterial infections by modulating the activity of bacterial proteins. The protein and antibody specific for it are useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases. The protein is useful for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense therapy and gene therapy. The present sequence is human IRAK4 DD protein

Sequence 98 AA;
Query Match 100.0%; Score 517; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e-60;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYRCLNVLGIRKLSDFIDPEGWKLAIVAIKPSGDRYNQPHIRFEALLQTGKSPTS 60
DB 1 TYRCLNVLGIRKLSDFIDPEGWKLAIVAIKPSGDRYNQPHIRFEALLQTGKSPTS 60
QY 61 ELFPDMGTNCTVGDVLDLIONEFPAPASLLPDVAVP 98
DB 61 ELFPDMGTNCTVGDVLDLIONEFPAPASLLPDVAVP 98

RESULT 2
ID AAE38897 standard; protein; 98 AA.
AC AAE38897;
XX
XX

DT 18-DEC-2003 (first entry)
XX
XX

DE Human IRAK4 DD protein.
XX

KW Human: death Domain; DD; death effector domain; DED; cell proliferation;
KW Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
KW neutral growth factor receptor-interacting protein; cell adhesion;
KW vasculotropic; microbial infection; inflammation; allograft rejection;
KW cell stress response; benign prostatic hyperplasia; antibacterial; NIDP;
KW apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
KW neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;
KW keloid; interleukin-1 receptor-associated kinase; IRAK.
XX

OS Homo sapiens.
XX

PN US2003049702-A1.
XX

PD 13-MAR-2003.
XX

PE 15-NOV-2001; 2001US-00001254.
XX

PR 17-NOV-2000; 2000US-00715893.
XX

PR 17-NOV-2000; 2000US-0367360P.
XX

PR 29-JUN-2001; 2001US-0301889P.
XX

PA (REED/) REED J C.
PA (GODZIK/) GODZIK A.
PA (PAWL/) PAWLOWSKI K.
PA (FLOR/) FLORENTINO L.
PA (LEES/) LEE S H.
PA (ROTH/) ROTH W.
PA (STEN/) STENNER-LIEWEN F.

XX Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
PI Steiner-Liwen F;
XX
XX WPI; 2002-500222/53.
DR N-PSDB; AAD59056.
XX
XX
PT New polypeptide comprising a death domain or death effector domain,
PT useful for discovery of drugs that suppress infection, inflammation,
PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
XX
PS Claim 1; Page 34; 99pp; English.

The present invention provides novel death Domain (DD) and death effector domain (DED) proteins and nucleic acids encoding them. The invention also provides death domain containing protein such as Chlamydia trachomatis death domain containing protein (CTDD) DD and neutral growth factor receptor-interacting death domain (NIDP) DD. The invention is useful for identifying a binding agent (e.g. protein or drug) that binds a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDP with a candidate that modulates the association of a DD, DED or NB-ARC domain with protein that binds the DD, DED or NB-ARC domain. The invention is also useful for modulating the level of cell process such as apoptosis, cell adhesion, cell proliferation, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching. DDEs and NB-ARC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are useful for discovery of drugs that suppress infection, autoimmunity, inflammation, allergy, allograft rejection, sepsis and other diseases. DD, DED or NB-ARC domain proteins are used to treat infection, allergy, hyperplasia, neoplasia, keloid, benign prostatic hyperplasia, fibrosis, inflammatory hyperplasia and smooth muscle cell proliferation in arteries following balloon angioplasty (restenosis). The invention is also used in antibody therapy and gene therapy. The present sequence is human interleukin-1 receptor-associated kinase (IRAK)-4 DD protein

Sequence 98 AA;

Query Match 100.0%; Score 517; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e-60;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYRCLNVLGIRKLSDFIDPEGWKLAIVAIKPSGDRYNQPHIRFEALLQTGKSPTS 60
DB 1 TYRCLNVLGIRKLSDFIDPEGWKLAIVAIKPSGDRYNQPHIRFEALLQTGKSPTS 60
QY 61 ELFPDMGTNCTVGDVLDLIONEFPAPASLLPDVAVP 98
DB 61 ELFPDMGTNCTVGDVLDLIONEFPAPASLLPDVAVP 98

RESULT 3
ID AAY92347 standard; protein; 206 AA.
AC AAY92347;
XX
XX

DT 10-AUG-2000 (first entry)
XX
XX

DE Human cancer associated antigen precursor from clone NY-BEN 64.
XX

KW renal cancer; cancer associated antigen precursor; diagnosis; cytostatic.
KW
KW
XX

OS Homo sapiens.
XX

PN WO200020587-A2.
XX

PD 13-APR-2000.
XX

PF 04-OCT-1999; 99WO-US022873.
XX

PR 05-OCT-1998; 98US-00166300.
XX

PR 05-OCT-1998; 98US-00166350.
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX
PI Obata Y, Gout I, Tureci O, Sahin U, Pfeundschnuh M, Scanlan MJ;
PI Stockert B, Chen Y, Old LJ, Jager B, Knuth A;
XX WPI; 2000-303774/26.
DR N-PSDB; AAA09319.
XX
PT Preventing, diagnosing and/or treating disorders associated with abnormal
PT expression of human cancer associated antigens.
XX
PS Example 1; Page 92-93; 121pp; English.
XX
CC AA92338-47 are encoded by novel genes isolated by SEREX screening from a
CC renal cancer cell line 1973/10.4. They are cancer associated antigen
CC precursors. These gene products are useful in methods for preventing,
CC diagnosing and/or treating disorders, especially cancer, associated with
CC abnormal expression of human cancer associated antigens. The method
CC comprises contacting a sample from a subject with an agent that
CC specifically binds to the nucleic acid molecule or expression product (or
CC fragment) complexed with a human leukocyte antigen (HLA) molecule and
CC determining the interaction between the agent and the nucleic acid
CC molecule or the expression product as a determination of the disorder
XX
SQ Sequence 206 AA;

Query Match 100.0%; Score 517; DB 3; Length 206;
Best Local Similarity 100.0%; Pred. No. 5.2e-60;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYVCLNVLGIRKLSDFIDPQGWKLAVALIKKPSGDRYNOFHRRFALLQTKSPTS 60
Db 9 TYVCLNVLGIRKLSDFIDPQGWKLAVALIKKPSGDRYNOFHRRFALLQTKSPTS 68
Qy 61 ELFPDWGTTNCTVGDVLDLIIQNEFPAPASLLPDPAVP 98
Db 69 ELFPDWGTTNCTVGDVLDLIIQNEFPAPASLLPDPAVP 106

RESULT 4
ABG12618
ID ABG12618 standard; protein; 455 AA.
XX
AC ABG12618;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #12609.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
FN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PP 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS76805.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

Claim 20; SEQ ID NO 42977; 103pp; English.

XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 455 AA;

Query Match 100.0%; Score 517; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.5e-59;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYVCLNVLGIRKLSDFIDPQGWKLAVALIKKPSGDRYNOFHRRFALLQTKSPTS 60
Db 9 TYVCLNVLGIRKLSDFIDPQGWKLAVALIKKPSGDRYNOFHRRFALLQTKSPTS 68
Qy 61 ELFPDWGTTNCTVGDVLDLIIQNEFPAPASLLPDPAVP 98
Db 69 ELFPDWGTTNCTVGDVLDLIIQNEFPAPASLLPDPAVP 106

RESULT 5
AAE24859
ID AAE24859 standard; protein; 460 AA.
XX
AC AAE24859;
XX
DT 22-OCT-2002 (first entry)
XX
DE Human IRAK4 protein #1.
XX
KW Human; death domain; DD; death effector domain; DED; Chlamydia infection;
KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;
KW inflammation; allergy; autoimmunity; allograft rejection; cell division;
KW immune-based pathology; fibrosis; arthritis; graft versus host disease;
KW immunosuppressive; gene therapy; antisense therapy.
XX
OS Homo sapiens.
XX
FN WO200240680-A2.
XX
PD 23-MAY-2002.
XX
PP 15-NOV-2001; 2001WO-US044844.
XX
PR 17-NOV-2000; 2000US-00715893.
PR 29-JUN-2001; 2001US-0301889P.
XX
PA (BURN-) BURNHAM INST.
XX
PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;

PI Stenmer-Liwen F;
 XX WPI; 2002-500222/53.
 DR N-PSDB; AAD40079.
 XX
 PT New polypeptide comprising a death domain or death effector domain,
 PT useful for discovery of drugs that suppress infection, inflammation,
 PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
 PS
 PS Claim 3; Page 183-184; 209pp; English.

XX The invention relates to an isolated polypeptide comprising a death
 CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention
 CC is useful for identifying a binding agent, preferably a protein or a drug
 CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC
 CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or
 CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and
 CC detecting the association of the domain and the candidate binding agent,
 CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or
 CC chemical crosslinking, nuclear magnetic resonance (NMR), mass
 CC spectroscopy (MS) and FPA. The invention is useful for modulating the
 CC level of a cell process such as cell proliferation, cell adhesion, cell
 CC stress responses, responses to microbial infection, cell apoptosis within a cell.
 CC Immunoglobulin class switching, in particular apoptosis within a cell.
 CC Antibody specifically reactive with CTDD DD of C. trachomatis, C.
 CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the
 CC CTDD DD protein is useful for detecting a Chlamydia infection. The
 CC invention is useful for modulating the activity of oncogenic proteins,
 CC for treating a pathology caused by the oncogenic proteins and for
 CC creating bacterial infections by modulating the activity of bacterial
 CC proteins. The protein and antibody specific for it are useful for
 CC discovery of drugs that suppress infection, inflammation, allergy,
 CC sepsis, autoimmunity, allograft rejection and other diseases. The protein
 CC is useful for treating immune-based pathologies, pathologies associated
 CC with cell division, inflammatory diseases such as sepsis, fibrosis,
 CC arthritis, graft versus host disease. The invention is used in antisense
 CC therapy and gene therapy. The present sequence is human IRAK4 protein
 XX
 SQ Sequence 460 AA;

Query Match 100.0%; Score 517; DB 5; Length 460;
 Best Local Similarity 100.0%; Pred. No. 1.6e-59;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TYVRCINVGILIRKLSDFIDPQEGWKKLAIVAIKRPSSGDDRYNQHRRFALLQTGKSPS 60
 DB 9 TYVRCINVGILIRKLSDFIDPQEGWKKLAIVAIKRPSSGDDRYNQHRRFALLQTGKSPS 68
 QY 61 ELFPDMGTNCTVGDVLDLILQNEFFAPASILLPDVAVP 98
 DB 69 ELFPDMGTNCTVGDVLDLILQNEFFAPASILLPDVAVP 106

RESULT 6
 AAE24865
 ID AAE24865 standard; protein; 460 AA.
 AC AAE24865;
 XX
 XX 22-OCT-2002 (first entry)
 DE Human IRAK4 protein #2.
 XX
 XX Human; death domain; DD; death effector domain; DED; Chlamydia infection;
 KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;
 KW inflammation; allergy; autoimmunity; allograft rejection; cell division;
 KW immune-based pathology; fibrosis; arthritis; graft versus host disease;
 KW immunosuppressive; gene therapy; antisense therapy.
 XX Homo sapiens.
 OS
 XX
 XX W0200240680-A2;

PD 23-MAY-2002.
 XX
 XX 15-NOV-2001; 2001WO-US044844.
 XX
 XX 17-NOV-2000; 2000US-00715893.
 PR 29-JUN-2001; 2001US-0301889P.
 XX
 PA (BURN-) BURHAM INST.
 XX
 PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W,
 PI Stenmer-Liwen F;
 XX
 DR WPI; 2002-500222/53.
 DR N-PSDB; AAD40085.
 XX
 PT New polypeptide comprising a death domain or death effector domain,
 PT useful for discovery of drugs that suppress infection, inflammation,
 PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
 PS
 PS Claim 1; Page 196-197; 209pp; English.

XX The invention relates to an isolated polypeptide comprising a death
 CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention
 CC is useful for identifying a binding agent, preferably a protein or a drug
 CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC
 CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or
 CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and
 CC detecting the association of the domain and the candidate binding agent,
 CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or
 CC chemical crosslinking, nuclear magnetic resonance (NMR), mass
 CC spectroscopy (MS) and FPA. The invention is useful for modulating the
 CC level of a cell process such as cell proliferation, cell adhesion, cell
 CC stress responses, responses to microbial infection and B cell
 CC immunoglobulin class switching, in particular apoptosis within a cell.
 CC Antibody specifically reactive with CTDD DD of C. trachomatis, C.
 CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the
 CC CTDD DD protein is useful for detecting a Chlamydia infection. The
 CC invention is useful for modulating the activity of oncogenic proteins,
 CC for treating a pathology caused by the oncogenic proteins and for
 CC creating bacterial infections by modulating the activity of bacterial
 CC proteins. The protein and antibody specific for it are useful for
 CC discovery of drugs that suppress infection, inflammation, allergy,
 CC sepsis, autoimmunity, allograft rejection and other diseases. The protein
 CC is useful for treating immune-based pathologies, pathologies associated
 CC with cell division, inflammatory diseases such as sepsis, fibrosis,
 CC arthritis, graft versus host disease. The invention is used in antisense
 CC therapy and gene therapy. The present sequence is human IRAK4 protein
 XX
 SQ Sequence 460 AA;

Query Match 100.0%; Score 517; DB 5; Length 460;
 Best Local Similarity 100.0%; Pred. No. 1.6e-59;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TYVRCINVGILIRKLSDFIDPQEGWKKLAIVAIKRPSSGDDRYNQHRRFALLQTGKSPS 60
 DB 9 TYVRCINVGILIRKLSDFIDPQEGWKKLAIVAIKRPSSGDDRYNQHRRFALLQTGKSPS 68
 QY 61 ELFPDMGTNCTVGDVLDLILQNEFFAPASILLPDVAVP 98
 DB 69 ELFPDMGTNCTVGDVLDLILQNEFFAPASILLPDVAVP 106

RESULT 7
 AAE38908
 ID AAE38908 standard; protein; 460 AA.
 AC AAE38908;
 XX
 XX 18-DEC-2003 (first entry)
 DE Human IRAK4 protein #2.
 XX
 XX

KW Human; death Domain; DD; death effector domain; DED; cell proliferation;
KW Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
KW neural growth factor receptor-interacting death domain; cell adhesion;
KW vasotropic; microbial infection; inflammation; allograft rejection; CTDD;
KW cell stress response; benign prostatic hypertrophy; antibacterial; NIDD;
KW apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
KW neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;
KW keloid; interleukin-1 receptor-associated kinase; IRAK.
XX
OS Homo sapiens.
XX
PN US2003049702-A1.
XX
PD 13-MAR-2003.
XX
PE 15-NOV-2001; 2001US-00001254.
XX
PR 17-NOV-2000; 2000US-00715893.
PR 17-NOV-2000; 2000US-0367360P.
PR 29-JUN-2001; 2001US-0301889P.
XX
PA (REED/) REED J C.
PA (GODZ/) GODZIK A.
PA (PAML/) PAWLOWSKI K.
PA (FIOR/) FIORENTINO L.
PA (LEES/) LEE S H.
PA (ROTH/) ROTH W.
PA (STEN/) STENNER-LIEWEN F.
XX
PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
PI Stenner-Liewen F;
XX
PI WPI: 2002-500222/53.
DR N-PSDB; AAD59067.
XX
PT New polypeptide comprising a death domain or death effector domain,
PT useful for discovery of drugs that suppress infection, inflammation,
PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
XX
PS Claim 1; Page 53-54; 99pp; English.
XX
CC The present invention provides novel death Domain (DD) and death effector
CC domain (DED) proteins and nucleic acids encoding them. The invention also
CC provides death domain containing protein such as Chlamydia trachomatis
CC death domain containing protein (CTDD) DD and neural growth factor
CC receptor-interacting death domain (NIDD) DD. The invention is useful for
CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED
CC or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate
CC binding agent and identifying an effective agent (e.g. protein or drug)
CC that modulates the association of a DD, DED or NB-ARC domain with protein
CC that binds the DD, DED or NB-ARC domain. The invention is also useful for
CC modulating the level of cell process such as apoptosis, cell adhesion,
CC cell proliferation, cell stress responses, responses to microbial
CC infection and B cell immunoglobulin class switching. DDs, DEDs and NB-ARC
CC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are
CC useful for discovery of drugs that suppress infection, autoimmunity,
CC inflammation, allergy, allograft rejection, sepsis and other diseases.
CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy,
CC autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte
CC hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,
CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries
CC following balloon angioplasty (restenosis). The invention is also used in
CC antibody therapy and gene therapy. The present sequence is human
CC Interleukin-1 receptor-associated kinase (IRAK)-4 protein
CC
XX
SQ Sequence 460 AA;
Query Match 100.0%; Score 517; DB 5; Length 460;
Best local Similarity 100.0%; Pred. No. 1.6e-55; Indels 0; Gaps 0;
Matches 98; Conservative 0; Mismatches 0;
1 TYVRCINLVGLIRKLSDFIDPOEGWKLAVALIKPESGDRYNOFHIRREALLOTGKSPTS 60
|||||

DB 9 TYVRCINLVGLIRKLSDFIDPOEGWKLAVALIKPESGDRYNOFHIRREALLOTGKSPTS 68
QY 61 ELFPDMGTNCTGYDLVDLILQNEFPAPASLLPDAVP 98
DB 69 ELFPDMGTNCTGYDLVDLILQNEFPAPASLLPDAVP 106
RESULT 8
AAE38902
ID AAE38902 standard; protein; 460 AA.
XX
AC AAE38902;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human IRAK4 protein #1.
XX
KW Human; death Domain; DD; death effector domain; DED; cell proliferation;
KW Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
KW neural growth factor receptor-interacting death domain; cell adhesion;
KW vasotropic; microbial infection; inflammation; allograft rejection; CTDD;
KW cell stress response; benign prostatic hypertrophy; antibacterial; NIDD;
KW apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
KW neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;
KW keloid; interleukin-1 receptor-associated kinase; IRAK.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 9..106
FT /note="Death domain of IRAK-4"
XX
PN US2003049702-A1.
XX
PD 13-MAR-2003.
XX
PE 15-NOV-2001; 2001US-00001254.
XX
PR 17-NOV-2000; 2000US-00715893.
PR 17-NOV-2000; 2000US-0367360P.
PR 29-JUN-2001; 2001US-0301889P.
XX
PA (REED/) REED J C.
PA (GODZ/) GODZIK A.
PA (PAML/) PAWLOWSKI K.
PA (FIOR/) FIORENTINO L.
PA (LEES/) LEE S H.
PA (ROTH/) ROTH W.
PA (STEN/) STENNER-LIEWEN F.
XX
PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
PI Stenner-Liewen F;
XX
PI WPI: 2002-500222/53.
DR N-PSDB; AAD59061.
XX
PT New polypeptide comprising a death domain or death effector domain,
PT useful for discovery of drugs that suppress infection, inflammation,
PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
XX
PS Claim 2; Fig 10B; 99pp; English.
XX
CC The present invention provides novel death Domain (DD) and death effector
CC domain (DED) proteins and nucleic acids encoding them. The invention also
CC provides death domain containing protein such as Chlamydia trachomatis
CC death domain containing protein (CTDD) DD and neural growth factor
CC receptor-interacting death domain (NIDD) DD. The invention is useful for
CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED
CC or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate
CC binding agent and identifying an effective agent (e.g. protein or drug)
CC that modulates the association of a DD, DED or NB-ARC domain with protein
CC that binds the DD, DED or NB-ARC domain. The invention is also useful for
CC modulating the level of cell process such as apoptosis, cell adhesion,
CC

CC cell proliferation, cell stress responses, responses to microbial
CC infection and B cell immunoglobulin class switching. Dbs, Dps and NB-ARC
CC domain and/or anti-DB, anti-DED or anti-NB-ARC domain antibodies are
CC useful for discovery of drugs that suppress infection, autoimmunity,
CC inflammation, allergy, allograft rejection, sepsis and other diseases.
CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy,
CC autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte
CC hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,
CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries
CC following balloon angioplasty (restenosis). The invention is also used in
CC antibody therapy and gene therapy. The present sequence is human
CC interleukin-1 receptor-associated kinase (IRAK)-4 protein
XX

Sequence 460 AA:

Query Match 100.0%; Score 517; DB 5; Length 460;
Best Local Similarity 100.0%; Pred. No. 1.6e-59;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYRCLNVGLIRKLSDFIDPQEGMKLAVALIKPSGDDRYNQFHRRFALLQTGKSPTS 60
DB 9 TYRCLNVGLIRKLSDFIDPQEGMKLAVALIKPSGDDRYNQFHRRFALLQTGKSPTS 68
61 ELFPDGTGTTCTVGDVLDLVLQNEFFAPASILLPDPAVP 98
69 ELFPDGTGTTCTVGDVLDLVLQNEFFAPASILLPDPAVP 106

Db 61 ELFPDGTGTTCTVGDVLDLVLQNEFFAPASILLPDPAVP 98
69 ELFPDGTGTTCTVGDVLDLVLQNEFFAPASILLPDPAVP 106

RESULT 9
ABR44401
ID ABR44401 standard; protein; 460 AA.
XX
AC ABR44401;
XX
DT 11-UTL-2003 (first entry)
DE Human IL-1 receptor-associated kinase-4 amino acid sequence.
XX
XX Antisense therapy; cytostatic; antimicrobial; antiinflammatory;
XX interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer;
XX inflammatory disease; infection; diagnostic; therapeutic; prophylaxis.
OS Homo sapiens.
XX
PN WO2003028636-A2.
XX
PD 10-APR-2003.
XX
PF 26-SEP-2002; 2002WO-US030574.
XX
PR 28-SEP-2001; 2001US-00966451.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett FC, Freiler SM;
PI
PI WPI; 2003-363256/34.
DR N-PSDB; ACC47548.
XX
XX

PT New antisense oligonucleotides for modulating IL-1 receptor-associated
PT kinase-4 gene expression, particularly useful for preventing, delaying or
PT treating e.g. cancer (e.g. renal cancer), inflammatory disease or an
PT infection.
XX
XX

PS Example 13; Page 80-83; 119pp; English.

CC The invention relates to a compound of 8-50 nucleobases which is targeted
CC to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated
CC kinase-4, specifically hybridizing with the nucleic acid and inhibiting
CC the expression of the encoded product. Also disclosed is the compound
CC hybridizing with an 8-nucleobase portion of an active site on a nucleic
CC acid molecule encoding IL-1 receptor-associated kinase-4. The antisense
CC oligonucleotide is useful for treating an animal having a disease or

CC conditions associated with IL-1 receptor-associated kinase-4, e.g. cancer
CC (particularly renal cancer), inflammatory disease or an infection. The
CC antisense compounds are useful for diagnostics, therapeutics,
CC prophylaxis, or as research reagents or kits. The current sequence
CC represents the human IL-1 receptor-associated kinase-4 amino acid
CC sequence
XX

Sequence 460 AA:

Query Match 100.0%; Score 517; DB 6; Length 460;
Best Local Similarity 100.0%; Pred. No. 1.6e-59;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYRCLNVGLIRKLSDFIDPQEGMKLAVALIKPSGDDRYNQFHRRFALLQTGKSPTS 60
DB 9 TYRCLNVGLIRKLSDFIDPQEGMKLAVALIKPSGDDRYNQFHRRFALLQTGKSPTS 68
61 ELFPDGTGTTCTVGDVLDLVLQNEFFAPASILLPDPAVP 98
69 ELFPDGTGTTCTVGDVLDLVLQNEFFAPASILLPDPAVP 106

RESULT 10
ADO44001
ID ADO44001 standard; protein; 460 AA.
XX
AC ADO44001;
XX
DT 15-UTL-2004 (first entry)
DE Amino acid sequence of human IRAK4.
XX
XX

XX protein complex; neurological disease; stroke; neurodegeneration;
XX Wallerian degeneration; Alzheimer's disease; neurological disorder;
XX epilepsy; inflammatory condition; ulcerative colitis; Crohn's disease;
XX atherosclerosis; 1D-MYO-inositol triphosphate 3 kinase A; ASK1; ASK2;
XX ASK3; CAMKII beta; CAMKII delta; CAMKII gamma; casein kinase II alpha;
XX Cdc37; CHK2; CTCL tumour antigen SE20-4; EF-1 alpha 1; EMAP;
XX FLJ14653 NT2R2002252; FLJ30839 PEBRA2002429; HERC2;
XX inositol polyphosphate-5-phosphatase; inositol-1; 4;
XX 5-triphosphate 5-phosphatase type 1; IRAK1; IRAK4; KIAA1441; MSTP030;
XX Nek3; Pak3; Pellino 1; Pellino 3; podocalyxin-like protein 1 precursor;
XX Pushover; 5-adenosylhomocysteinease;
XX secretory carrier-associated membrane protein 2; sufcelt locus protein 2;
XX ubiquitin carboxyl terminal hydrolase 11;
XX upstream regulatory element binding protein 1; Vartul;
XX Werner's syndrome helicase interacting protein; WHIP;
XX X-ray repair cross complementing protein 4.
XX

Homo sapiens.

WO2004031242-A2.

15-APR-2004.

11-SEP-2003; 2003WO-EP010110.

12-SEP-2002; 2002EP-00020495.

12-SEP-2002; 2002EP-00020496.

12-SEP-2002; 2002EP-00020497.

(CELL-) CELLZOME AG.

WPI; 2004-316467/29.

CC New complex comprising at least one first protein, and at least one
CC second protein, useful for treating stroke, Alzheimer's disease,
CC neurological disorders such as epilepsy, and inflammatory conditions such
CC as ulcerative colitis.
XX

PS Example, Page 213-214, 287pp; English.

XX The specification describes protein complexes involved in cellular
 CC processes which have been shown to be critical for the development of
 CC various forms of neurological diseases. Three protein complexes were
 CC identified: ASK2 protein complex, Pellino-1 protein complex and Pellino-3
 CC protein complex. The protein complex are useful for treating diseases and
 CC disorders, e.g. stroke, neurodegeneration such as Wallerian degeneration,
 CC Alzheimer's disease, neurological disorders such as epilepsy, and
 CC inflammatory conditions such as ulcerative colitis, Crohn's disease or
 CC atherosclerosis. Proteins identified as being part of the protein
 CC complexes of the invention are ID-MYO-inositol triphosphate 3 kinase A,
 CC ASK1, ASK2, ASK3, CamKII beta, CamKII gamma, casein kinase
 CC II alpha, Cdc37, CHK2, CTCL tumour antigen SE20-4, EF-1 alpha 1, EMAP,
 CC FLJ14653 NT2RP2002252, FLJ30839 FEBRA2002429, HERC2, two hypothetical
 CC proteins of 35.5 kDa and 49.3 kDa, inositol polyphosphate-5-phosphatase,
 CC inositol-1,4,5-triphosphate 5-phosphatase type 1, IRAK1, IRAK4, KIAA1411,
 CC MSP030, Nek9, PAR3, Pellino 1, Pellino 3, podocalyxin-like protein 1
 CC precursor, Pushover, a putative S-adenosylhomocysteine, secretory
 CC carrier-associated membrane protein 2, surfact locus protein 2, ubiquitin
 CC carboxyl terminal hydrolase 11, upstream regulatory element binding
 CC protein 1, Vartul, Werner's syndrome helicase interacting protein (WHIP),
 CC X-ray repair cross complementing protein 4 (isoform 1). The present
 CC sequence represents IRAK4.

XX SQ Sequence 460 AA;

Query Match 100.0%; Score 517; DB 8; Length 460;
 Best Local Similarity 100.0%; Pred. No. 1.6e-55;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYVCLNVLGRLKSDFLDPGKGLAVAIKPSGDRYNOFHIRREALLQTSKSTS 60
 Db 9 TYVCLNVLGRLKSDFLDPGKGLAVAIKPSGDRYNOFHIRREALLQTSKSTS 68

Qy 61 ELFPDWGTTNCTVGDVLDLIIQNEFPAPASLLPDAVP 98
 Db 69 ELFPDWGTTNCTVGDVLDLIIQNEFPAPASLLPDAVP 106

RESULT 11
 AAE05402
 ID AAE05402 standard; protein, 191 AA.
 XX
 AC AAE05402;
 DT 24-SEP-2001 (first entry)
 XX
 DE Truncated form of human IRAK-4 protein.
 XX
 KM Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytosolic;
 KM IL; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD;
 KM chronic obstructive pulmonary disease; neuroprotective; chronic cough;
 KM adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS;
 KM interstitial lung disease; allergic rhinitis; transplant rejection;
 KM autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KM multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke;
 KM cardiovascular disease; atherosclerosis; neurodegenerative disease;
 KM sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis;
 KM inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis;
 KM Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor;
 KM sarcoidosis; transgenic animal; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN MO200151641-A1.
 XX
 PD 19-JUL-2001.
 XX
 PF 12-JAN-2001, 2001WO-US001171.
 XX
 PR 13-JAN-2000, 2000US-0176395P.

XX (TULIA-) TULARIX INC.
 PA
 XX
 PI Mesche H, Ld S;
 XX
 DR WPI; 2001-451860/48.
 XX
 PR Novel human interleukin-1 receptor associated kinase polypeptide, useful
 PT for identifying modulators of the polypeptide for treating gout, asthma,
 PT allergic rhinitis, multiple sclerosis and skin cancer.
 XX
 PS Claim 53; Page; 89pp; English.

XX The patent discloses interleukin (IL)-1 receptor associated kinase (IRAK)
 CC -4 proteins and their cDNAs. IRAK associate with activated IL-1, IL-18
 CC and other receptors and act to transduce signals originating from the
 CC activated receptors, ultimately leading to a variety of downstream
 CC effects such as nuclear factor (NF)-kappa activation. The IRAK-4
 CC inhibitors are useful for treating inflammatory diseases such as
 CC pulmonary diseases and diseases of the airway (e.g., adult respiratory
 CC disease syndrome (ARDS), chronic obstructive pulmonary disease (COPD),
 CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or
 CC allergic rhinitis), transplant rejection, autoimmune diseases (e.g.,
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or
 CC diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma),
 CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of
 CC the central nervous system (e.g., neurodegenerative disease), CD14
 CC mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis,
 CC psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic
 CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and
 CC ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout,
 CC sarcoidosis and ophthalmic diseases and conditions. The inhibitors of
 CC IRAK-4 in vivo, to generate models for the study of inflammatory
 CC disorders and conditions and for the development of potential treatments
 CC for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences
 CC are also used in gene therapy and in antisense therapy. The present
 CC sequence is the truncated form of human IRAK-4 protein. This sequence was
 CC constructed by deleting the residues after K191 in the wild type human
 CC IRAK-4 protein. This truncated form is the dominant negative form of
 CC human IRAK-4 protein. Note: This sequence is not shown in the
 CC specification but is derived from human IRAK-4 (SEQ ID NO: 1) shown in
 CC figure 1 of the specification (AAE05398)

XX SQ Sequence 191 AA;

Query Match 99.2%; Score 513; DB 4; Length 191;
 Best Local Similarity 99.0%; Pred. No. 1.6e-55;
 Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TYVCLNVLGRLKSDFLDPGKGLAVAIKPSGDRYNOFHIRREALLQTSKSTS 60
 Db 9 TYVCLNVLGRLKSDFLDPGKGLAVAIKPSGDRYNOFHIRREALLQTSKSTS 68

Qy 61 ELFPDWGTTNCTVGDVLDLIIQNEFPAPASLLPDAVP 98
 Db 69 ELFPDWGTTNCTVGDVLDLIIQNEFPAPASLLPDAVP 106

RESULT 12
 AAE05398
 ID AAE05398 standard; protein, 460 AA.
 XX
 AC AAE05398;
 DT 24-SEP-2001 (first entry)
 XX
 DE Human interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 protein.

Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytostatic; IL; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD; chronic obstructive pulmonary disease; neuroprotective; chronic cough; adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease; allergic rhinitis; transplant rejection; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; multibody sclerostis; diabetes; cancer; solid tumour; lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis; inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis; Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor; sarcoidosis; transgenic animal.

Homo sapiens.

Key Location/Qualifiers
 Domain 5..147
 /label= Death domain
 /note= "Also known as N-terminal domain"
 Domain 192..460
 /label= Central_kinase_domain

MO200151641-A1.

19-JUL-2001.

12-JAN-2001; 2001WO-US001171.

13-JAN-2000; 2000US-0176395P.

(TULIA-) TULARIK INC.

Wesche H, Li S;
 WPI; 2001-451860/48.
 N-PSDB; AAD10197.

Novel human interleukin-1 receptor associated kinase polypeptide, useful for identifying modulators of the polypeptide for treating gout, asthma, allergic rhinitis, multiple sclerosis and skin cancer.

Claim 17; Fig 1; 89pp; English.

The present sequence is human interleukin (IL)-1 receptor associated kinase (IRAK)-4 protein. IRAK associate with activated IL-1, IL-18 and other receptors and act to transduce signals originating from the activated receptors, ultimately leading to a variety of downstream effects such as nuclear factor (NF)-kappa activation. The IRAK-4 inhibitors are useful for treating inflammatory diseases such as pulmonary diseases and diseases of the airway (e.g., adult respiratory pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or allergic rhinitis), transplant rejection, autoimmune diseases (e.g., rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma), cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of the central nervous system (e.g., neurodegenerative disease), CD14 mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis, psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic dermatitis), inflammatory bowel disease (e.g., Crohn's disease and sarcoidosis) and ophthalmic diseases and conditions. The inhibitors of IRAK-4 activity or expression are used to inhibit signal transduction resulting from the activation of an interleukin-1 receptor (IL-1R)/Toll receptor in a cell. They also inhibit the activation of a transcription factor that activates NFkappa in the cell. IRAK-4 is used to create a nonhuman transgenic animal which is useful for testing the function of IRAK-4 in vivo, to generate models for the study of inflammatory disorders and conditions and for the development of potential treatments for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences are also used in gene therapy and in antisense therapy.

Sequence 460 AA;

Query Match 99.2%; Score 513; DB 4; Length 460;
 Best Local Similarity 99.0%; Pred. No. 5.3e-59;
 Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TYRCLNVGIRLSPFIDPOEGMKLAIAIKPSGDDRYNPFIRREALLQTKSPTS 60
 9 TYRCLNVGIRLSPFIDPOEGMKLAIAIKPSGDDRYNPFIRREALLQTKSPTS 68

61 ELFPDGTNCTVGDVLDLIIQNEFPAPASLLPDAVP 98
 69 ELFPDGTNCTVGDVLDLIIQNEFPAPASLLPDAVP 106

RESULT 13
 AAB05401
 ID AAB05401 standard; protein; 460 AA.
 AC AAB05401;
 XX
 XX 24-SEP-2001 (first entry)
 DT
 XX
 XX Human IRAK-4 mutant (K213A, K214A).
 DE
 XX
 XX Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytostatic; IL; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD; chronic obstructive pulmonary disease; neuroprotective; chronic cough; adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease; allergic rhinitis; systemic lupus erythematosus; autoimmune disease; rheumatoid arthritis; transplant rejection; multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis; inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis; Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor; sarcoidosis; transgenic animal; mutant; mutein.

OS Homo sapiens.
 OS Synthetic.

Key Location/Qualifiers
 FT Misc-difference 213 /note= "Wild type Lys substituted with Ala"
 FT Misc-difference 214 /note= "Wild type Lys substituted with Ala"
 FT
 XX
 XX MO200151641-A1.
 XX
 XX 19-JUL-2001.
 XX
 XX 12-JAN-2001; 2001WO-US001171.
 XX
 XX 13-JAN-2000; 2000US-0176395P.
 XX
 XX (TULIA-) TULARIK INC.
 XX
 XX Wesche H, Li S;
 XX WPI; 2001-451860/48.
 XX
 XX Novel human interleukin-1 receptor associated kinase polypeptide, useful for identifying modulators of the polypeptide for treating gout, asthma, allergic rhinitis, multiple sclerosis and skin cancer.

Claim 51; Page; 89pp; English.

The patent discloses interleukin (IL)-1 receptor associated kinase (IRAK)-4 proteins and their cDNAs. IRAK associate with activated IL-1, IL-18 and other receptors and act to transduce signals originating from the activated receptors, ultimately leading to a variety of downstream effects such as nuclear factor (NF)-kappa activation. The IRAK-4 inhibitors are useful for treating inflammatory diseases and conditions such as pulmonary diseases and diseases of the airway (e.g., adult respiratory

CC disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD),
 CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or
 CC allergic rhinitis), transplant rejection, autoimmune diseases (e.g.,
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or
 CC diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma),
 CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of
 CC the central nervous system (e.g., neurodegenerative disease), CD14
 CC mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis,
 CC psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic
 CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and
 CC ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout,
 CC sarcoidosis and ophthalmic diseases and conditions. The inhibitors of
 CC IRAK-4 activity or expression are used to inhibit signal transduction
 CC resulting from the activation of an interleukin-1 receptor (IL-1R)/Toll
 CC receptor in a cell. They also inhibit the activation of a transcription
 CC factor that activates NFkappaB in the cell. IRAK-4 is used to create a
 CC nonhuman transgenic animal which is useful for testing the function of
 CC IRAK-4 in vivo, to generate models for the study of inflammatory
 CC disorders and conditions and for the development of potential treatments
 CC for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences
 CC are also used in gene therapy and in antisense therapy. The present
 CC sequence is a mutant (K213A, K214A) of human IRAK-4 protein. Note: This
 CC sequence is not shown in the specification but is derived from human IRAK
 CC -4 (SEQ ID NO: 1) shown in figure 1 of the specification (AA05398)
 CC
 XX SQ Sequence 460 AA;

Query Match 99.2%; Score 513; DB 4; Length 460;
 Best Local Similarity 99.0%; Pred. No. 5.3e-59;
 Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TYVCLNGLIRKISDFIDPOGKGLAVAIKKPSGDRYQFHRFEALLQTKSPTS 60
 Db 9 TYVCLNGLIRKISDFIDPOGKGLAVAIKKPSGDRYQFHRFEALLQTKSPTS 68
 QY 61 ELTFDWTGTTNCTAGDVLVDLIQNEFPAPASILLDPDVP 98
 Db 69 ELTFDWTGTTNCTAGDVLVDLIQNEFPAPASILLDPDVP 106

RESULT 14
 AA05403
 ID AA05403 standard; protein; 460 AA.
 XX
 AC AA05403;

XX 24-SEP-2001 (first entry)

DE Human IRAK-4 polymorphic variant (I531L).

XX Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytosolic;
 KM IL; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD;
 KM chronic obstructive pulmonary disease; neuroprotective; chronic cough;
 KM adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS;
 KM interstitial lung disease; allergic rhinitis; transplant rejection;
 KM autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KM multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke;
 KM cardiovascular disease; atherosclerosis; neurodegenerative disease;
 KM sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis;
 KM inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis;
 KM Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor;
 KM sarcoidosis; transgenic animal; mutant; mutein; variant; polymorphism.
 XX

OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 53 /note= "Wild type Ile substituted with Leu"

XX WO200151641-A1.

XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-US001171.
 PF
 XX 13-JAN-2000; 2000US-0176395P.
 PR
 XX (TTLA-) TTLARIK INC.
 PA
 XX Wesche H, Li S;
 PI
 XX WPI; 2001-451860/48.
 DR

PT Novel human interleukin-1 receptor associated kinase polypeptide, useful
 PT for identifying modulators of the polypeptide for treating gout, asthma,
 PT allergic rhinitis, multiple sclerosis and skin cancer.

PS Disclosure; Page; 89pp; English.

XX The patent discloses interleukin (IL)-1 receptor associated kinase (IRAK)
 CC -4 proteins and their cDNAs. IRAK associate with activated IL-1, IL-18
 CC and other receptors and act to transduce signals originating from the
 CC activated receptors, ultimately leading to a variety of downstream
 CC effects such as nuclear factor (NF)-kappaB activation. The IRAK-4
 CC inhibitors are useful for treating inflammatory diseases such as
 CC pulmonary diseases and diseases of the airway (e.g., adult respiratory
 CC disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD),
 CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or
 CC allergic rhinitis), transplant rejection, autoimmune diseases (e.g.,
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or
 CC diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma),
 CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of
 CC the central nervous system (e.g., neurodegenerative disease), CD14
 CC mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis,
 CC psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic
 CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and
 CC ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout,
 CC sarcoidosis and ophthalmic diseases and conditions. The inhibitors of
 CC IRAK-4 activity or expression are used to inhibit signal transduction
 CC resulting from the activation of an interleukin-1 receptor (IL-1R)/Toll
 CC receptor in a cell. They also inhibit the activation of a transcription
 CC factor that activates NFkappaB in the cell. IRAK-4 is used to create a
 CC nonhuman transgenic animal which is useful for testing the function of
 CC IRAK-4 in vivo, to generate models for the study of inflammatory
 CC disorders and conditions and for the development of potential treatments
 CC for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences
 CC are also used in gene therapy and in antisense therapy. The present
 CC sequence is a polymorphic variant (I531L) of human IRAK-4 protein. Note:
 CC This sequence is not shown in the specification but is derived from human
 CC IRAK-4 (SEQ ID NO: 1) shown in figure 1 of the specification (AA05398)
 CC
 XX SQ Sequence 460 AA;

Query Match 98.8%; Score 511; DB 4; Length 460;
 Best Local Similarity 98.0%; Pred. No. 9.9e-59;
 Matches 96; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TYVCLNGLIRKISDFIDPOGKGLAVAIKKPSGDRYQFHRFEALLQTKSPTS 60
 Db 9 TYVCLNGLIRKISDFIDPOGKGLAVAIKKPSGDRYQFHRFEALLQTKSPTS 68
 QY 61 ELTFDWTGTTNCTAGDVLVDLIQNEFPAPASILLDPDVP 98
 Db 69 ELTFDWTGTTNCTAGDVLVDLIQNEFPAPASILLDPDVP 106

RESULT 15

AA05404
 ID AA05404 standard; protein; 460 AA.

XX AA05404;

XX 24-SEP-2001 (first entry)

DE Human IRAK-4 polymorphic variant (G17A).

XX Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytosolic;
 KW IL; antibacterial; antiinflammatory; ophthalmological; vasotrophic; OPD;
 KW chronic obstructive pulmonary disease; neuroprotective; chronic cough;
 KW adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS;
 KW interstitial lung disease; allergic rhinitis; transplant rejection;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke;
 KW cardiovascular disease; atherosclerosis; neurodegenerative disease;
 KW sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis;
 KW inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis;
 KW Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor;
 KW sarcoidosis; transgenic animal; mutant; mutein; variant; polymorphism.
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 17 /note= "Wild type Gly substituted with Ala"
 PT
 PN WO200151641-A1.
 PN 19-JUL-2001.
 XX
 XX 12-JAN-2001; 2001WO-US001171.
 XX
 XX 13-JAN-2000; 2000US-0176395P.
 XX
 XX (TULSA-) TULARIK INC.
 XX
 XX Mesche H, Li S;
 XX WPI; 2001-451860/48.
 DR
 PT Novel human interleukin-1 receptor associated kinase polypeptide, useful
 PT for identifying modulators of the polypeptide for treating gout, asthma,
 PT allergic rhinitis, multiple sclerosis and skin cancer.
 XX
 PS Disclosure; Page: 89pp; English.

SQL Sequence 460 AA;
 Query Match 98.1%; Score 507; DB 4; Length 460;
 Best Local Similarity 98.0%; Pred. No. 3.4e-58;
 Matches 96; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TYRCLAVGLIRKLSPIFDPQSGKKLAVAIKKPSGDRYQFHIRREALLQTKSPPTS 60
 DB 9 TYRCLAVGLIRKLSPIFDPQSGKKLAVAIKKPSGDRYQFHIRREALLQTKSPPTS 68
 QY 61 ELTFDWTGNTCTGVDDVLDLIONEFPAPASLLPDVAVP 98
 DB 69 ELTFDWTGNTCTGVDDVLDLIONEFPAPASLLPDVAVP 106
 Search completed: January 10, 2005, 23:21:49
 Job time : 155 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	75.5	14.6	257	2	D69877	unpoporphylin-III C
2	72	13.9	252	2	A33170	tube protein - frn
3	71	13.7	252	2	A24700	apolipoprotein A-I
4	67.5	13.1	257	2	B64626	type I restriction
5	67	13.0	334	2	A10284	probable exported
6	67	13.0	355	2	C64714	translational elong
7	66.5	12.9	299	2	S76848	hypothetical prot
8	66.5	12.9	491	2	B96633	hypothetical prot
9	66.5	12.9	579	2	T50228	conserved hypothe
10	66.5	12.9	2809	2	T30213	G-cadherin sea v
11	66	12.8	598	2	A82839	hypothetical prote
12	65	12.6	355	2	G71804	translational elong
13	65	12.6	440	2	D95952	probable glycosyl
14	64.5	12.5	662	2	JC7906	sucrose 1F-fructo
15	64	12.4	122	2	G82217	probable 6-pyruvo
16	64	12.4	501	2	S76581	hypothetical prot
17	64	12.4	516	2	T52611	glucose-6-phosphat
18	63.5	12.3	388	2	T32153	hypothetical prot
19	63.5	12.3	501	2	A45775	hypothetical prot
20	62.5	12.2	621	2	T18777	protein kinase p11
21	62.5	12.1	220	2	G70529	hypothetical prot
22	62.5	12.1	256	2	A12344	probable trkB pro
23	62.5	12.1	459	2	A35291	two-component syst
24	62.5	12.1	478	2	D72344	adenylousuccinate
25	62.5	12.1	1423	1	T37275	DNA polymerase II
26	62.5	12.1	1674	2	T01265	death-associated fl
27	62	12.0	265	1	LPR81B	starch synthase nu
28	62	12.0	266	1	LPR81Z	apolipoprotein A-I
29	62	12.0	693	2	B84647	hypothetical prote

30	62	12.0	746	2	T29588	hypothetical prote
31	62	12.0	755	2	G90996	probable host spec
32	62	12.0	782	2	A85693	hypothetical prote
33	62	12.0	807	2	B85631	hypothetical prote
34	62	12.0	808	2	G90968	host specificity p
35	62	12.0	977	2	B85741	hypothetical prote
36	62	12.0	1157	2	A97769	probable host spec
37	62	12.0	1158	2	F90854	probable host spec
38	62	12.0	1158	2	G85718	probable host comp
39	62	12.0	1159	2	A90899	probable tail spec
40	62	12.0	1159	2	G85816	hypothetical prote
41	62	12.0	1165	2	B85842	probable tail fibre
42	62	12.0	1165	2	F90877	probable host spec
43	61.5	11.9	152	2	F98259	probable transcrip
44	61.5	11.9	152	2	AC3025	transcription regu
45	61.5	11.9	293	2	JQ1701	hypothetical 33.2K

ALIGNMENTS

[illegible]

Proc. Natl. Acad. Sci. U.S.A. 88, 810-814, 1991
A>Title: Genetic and molecular characterization of tube, a *Drosophila* gene maternally repressed in the embryo
A:Reference number: A37662; MUID:91126085; PMID:189484
A:Accession: A37662
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-462 <LET>
A:Cross-references: UNIPROT:P22812; GB:M59501; NID:g158750; PID:g158751
C:Genetics:
A:Gene: FlyBase:tnb
A:Cross-references: FlyBase:FBgn0003882
C:Superfamily: Drosophila tube protein

	Query Match	13.9%;	Score 72;	DB 2;	length 462;
	Best Local Similarity	24.8%;	Pred. No. 4;		
	Matches	28;	Conservative 16;	Mismatches 39;	Indels 30; Gaps 4
QY	11 IRKLSDFIDPQGEMKLAAVAKIKPSGDD-----RY--NQFHRR	47			
Db	41 IYRLAKIIDENSCMKLMSIT--PKGMDOAQCSGAGCINFPAEIKKGFFYTADVFQIDE	98			
QY	48 FEALLIQTSKPTSELLFDWGT-----NCTVDLDVLILIONFEFAPASULLPD	95			
Db	99 AANRLPPDQSQKMIMDEWKISGKNLERPTVGVLQLLVQAELFEAADFVALD	151			

RESULT 3
A24700
apolipoprotein A-I precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C/Accession: A24700; S00298; A05314
R/Haddad, I.A.; Otdovsky, J.M.; Fitzpatrick, T.; Karathanasis, S.K.
J. Biol. Chem. 261, 13268-13277, 1986
A>Title: Linkage, evolution, and expression of the rat apolipoprotein A-I, C-III, and A-II
A/Accession: A92558; MUID:87008540; PMID:3020028
A/Molecule type: DNA
A/Residues: 1-259 <HMD>
A/Cross-references: UNIPROT:P04639; EMBL:J02597; NID:g202935; PIDN:AAA0745.1; PID:g202935
R/Ponchik, J.E.; Martini, J.A.; Giesen, J.E.
Eur. J. Biochem. 140, 493-498, 1984
A>Title: Cloning and structure analysis of the rat apolipoprotein A-I cDNA.
A/Reference number: S00298; MUID:A4207897; PMID:643662

A:Accession: S00298
A:Molecule type: mRNA
A:Residues: 1-259 <PON>
A:Cross-references: GB:M00001; EMBL:X00558; NID:g202944; PIDD:AAA40749.1; PID:g202945
R:Gordon, J.I.; Smith, D.P.; Andy, R.; Alpers, D.H.; Schonfeld, G.; Strauss, A.W.
J. Biol. Chem. 1977, 971-978, 1982
A:Title: The primary translation product of rat intestinal apolipoprotein A-I mRNA is a
A:Reference number: A05314; MUID:82098162; PMID:6798036
A:Accession: A05314
A:Molecule type: protein
A:Residues: 1-18, 'X', '20-21, 'X', '23-28, 'X', '30-38, 'X', '40-41, 'X', '43-45 <GOR>
C:Comment: This protein is synthesized in the liver and small intestine. The propeptide
C:Comment: This protein is a major component of the high density lipoproteins in plasma.
C:Genetics:
A:introns: 15/1; 66/2
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipid
F:1-18/Domain: signal sequence #status experimental <STG>
F:19-24/Domain: propeptide #status experimental <PRO>
F:25-259/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 13.7%; Score 71; DB 2; Length 259;
 Best Local Similarity 31.2%; Pred. No. 2.5;
 Matches 24; Conservative 8; Mismatches 31; Indels 14; Gaps 3

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QY      19 DPQSGWKLA-----VAIKPSGDRYNOFHIRFALLQTKSPTEELLEFDNCTNCT 72
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      26 EPQSGQMRVNDFAIYYVDVAVDSCGDVYSQESSSTL-----GRQNLNLNDMDTLGST 79

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QY 73 VGDVLDL--IQNEFFA 87
||| : | ||:
Db 80 VGRLEQLGPVTQEFWA 96

RESULT 4

type I restriction enzyme M protein - *Helicobacter pylori* (strain 26695)
C:Species: *Helicobacter pylori*

```

#sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:\Accession: B64626

```

Peterson, S.; Loft
Bon J. D.; Kelley

A;Authors: Wallin,

A/Reference number: A64520; MUID:97394467; PMID:9252185

A;status: preliminary
A;molecule type: DN

A:Cross-references: UNIPROT:Q25521; GB:AE000596; GB:AE000511; NID:q2313982; PTDN:AD0789-

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	52
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Best Local Similarity 31.1%; Pred. No. 15;
Matches 19; Conservative 11; Mismatches 28; Indels 3; Gaps 1.

QY 37 DDRYNQHIRFEALL--QTGKSPTELLFDWGTNCTVGDVLVDLLIQNEFFAPASLLL 93

2/9 DINYSKFHIAHGDILLDPKHEDEPFDAIVSNPPYSTKVGDSNPILINDERFSPAGVLA 338

Db 339 P 339

RESULT 5
AI0284

C:/Species: Yersinia pestis
C:/Date: 03-Nov-2001 #Accession: 980607

C/Accession: A10284
R;Parkhill, J.: Wren, B.W.: Thomson, N.R.: Titball P.W.: Wolfer M.E.C.

il, M.; Rutherford,

A:1:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague
A:Reference number: AB00001: MIMD:21470413: DWT:150330

A;Status: preliminary

A;Residues: 1-334 <K
A:Cross-references:

A; Gene: YPO2336

Query Match	Score	DB	Length
13.0%	67	2	334

Matches	22;	Conservative	11;	Mismatches	24;	Indels	26;	Gaps	3;
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76 LUDLOWEEN, R. C. 1963. 2

255 -----

1
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3
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264714

translation elongation factor EF-Ts - Helicobacter pylori (strain 26695)
 C/Species: Helicobacter pylori
 C/Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
 C/Accession: G64714
 R/Tomb, J.R.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khajak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997
 A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpi, P.D.; Smith, H.O.; Fraser, C.
 A/Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A/Reference number: A64520; MUID:97394467; PMID:9252185
 A/Accession: G64714
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-355 <TOM>
 A/Cross-references: UNIPROT:P55975; GB:AE000653; GB:AE000511; NID:g2314733; PIDN:AA00855
 C/Superfamily: translation elongation factor EF-Ts

Query Match 13.0%; Score 67; DB 2; Length 355;
 Best Local Similarity 22.9%; Pred. No. 11;
 Matches 24; Conservative 17; Mismatches 34; Indels 30; Gaps 3;
 Oy 11 IRKLSDFIDPQBGWKKLAVALIKPSGDDRYNOFH-----RRFEALLQTG----- 55
 Db 78 INSERTFVAKNEGFKEL--VKKTLETTKANHHTTEELLKSPDKNKFEETLHSGIAVI 134
 Oy 56 -----KSPTSELFPDWGTTCTGVDLVLLIQNEFPAP 88
 Db 135 GENILVRKIALHKAPESSHIINGYAHSNARVGLIGIKTDNEKNAP 179

RESULT 7
 576848
 hypothetical protein - Synechocystis sp. (strain PCC 6803)
 C/Species: Synechocystis sp.
 A/Variety: PCC 6803
 C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C/Accession: S76848
 R/Kaneke, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
 A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.
 A/Reference number: S74322; MUID:97061201; PMID:8905231
 A/Accession: S76848
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-299 <KAN>
 A/Cross-references: UNIPROT:P74644; EMBL:D90917; GB:AB001339; NID:G1653836; PIDN:BA1876
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C/Genetics:
 A/Start codon: GTG

Query Match 12.9%; Score 66.5; DB 2; Length 299;
 Best Local Similarity 28.4%; Pred. No. 9.8;
 Matches 23; Conservative 16; Mismatches 37; Indels 5; Gaps 3;
 Oy 12 RKLSDFIIDPQBGWKKLAVALIKPSGDDRYNOFHRRFEALLQTGKSPSELFPDWGTTN 70
 Db 159 RRLADKLKERLGY--LGYVYKRPKPS--HFYRNFSPOEKQEVLEDSQYREIILISYFDE 214
 Oy 71 CTGVDLVLLIQNEFPAPASL 91
 Db 215 GTVNDLDDQFVNOAFADLAI 235

RESULT 8
 B96633
 hypothetical protein F8A5.28 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: B96633
 R/Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Hultzar, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: B96633
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-491 <STO>
 A/Cross-references: UNIPROT:O22714; GB:AE005173; NID:g2462744; PIDN:AA871963.1; GSPDB:GN
 C/Genetics:
 A/Gene: F8A5.28
 A/Map position: 1

Query Match 12.9%; Score 66.5; DB 2; Length 491;
 Best Local Similarity 26.3%; Pred. No. 18;
 Matches 20; Conservative 15; Mismatches 34; Indels 7; Gaps 2;
 Oy 8 VGLRKLSDFIDPQBGWKKLAVALIKPSGDDRYNOFHRRFEALLQTGKSPSELFPDWG 67
 Db 271 ITLVGRGLKLTREYRIWRSLRLAIPTK-----NVAYLNMIOVLKLDLPGAEITLFEW 325
 Oy 68 TTNCVGD--LVYDLI 81
 Db 326 QANCSYDIRIVNLI 341

RESULT 9
 T50228
 conserved hypothetical protein SPAC607.08c [imported] - fission yeast (Schizosaccharomyces pombe)
 C/Species: Schizosaccharomyces pombe
 C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
 C/Accession: T50228
 R/Zimmermann, W.; Wandut, R.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, December 1999
 A/Reference number: Z25047
 A/Accession: T50228
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-579 <ZIM>
 A/Cross-references: UNIPROT:Q9US10; EMBL:AL135751; PIDN:CAB63795.1; GSPDB:GN00066; SPDB: A/Experimental source: strain 972h(-); comid c607
 C/Genetics:
 A/Gene: SPDB:SPAC607.08c
 A/Map position: 1
 C/Superfamily: Caenorhabditis elegans hypothetical protein F35D11.3

Query Match 12.9%; Score 66.5; DB 2; Length 579;
 Best Local Similarity 30.8%; Pred. No. 22;
 Matches 28; Conservative 13; Mismatches 39; Indels 11; Gaps 5;
 Oy 6 LNVGLIRKLSDFIDPQBGWKKLAVALIKPSGDDRYN-QFHRRFEALLQTGKSPSELFP 64
 Db 268 VTIGISGWLGDYNEVDAMKSLTVGDKSYWGDYALKFEV--EALVDLQKS--LSRLIF 323
 Oy 65 DWGTTCTGVDLVLLIQNEFPAP-ASLLLP 94
 Db 324 SAG-----LGMVKGSEVISRTILAPLAAALWP 349

RESULT 10
 T30213
 G-caderlin - sea urchin (Lytechinus variegatus)
 C/Species: Lytechinus variegatus (variegated urchin)
 C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T30213
 R/Miller, J.R.; McClay, D.R.
 Dev. Biol. 192, 323-339, 1997

A>Title: Characterization of the role of cadherin in regulating cell adhesion during seed
A/Reference number: Z20780; MUID:98104238; PMID:9441671
A/Accession: T30213
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-2809 <MIL>
A/Cross-references: UNIPROT:061230; EMBL:U34823; NID:g2982186; PID:g2982187; PIDN:MAC063

Query Match 12.9%; Score 66.5; DB 2; Length 2809;
Best Local Similarity 32.4%; Pred. No. 1.5e+02;
Matches 24; Conservative 12; Mismatches 35; Indels 3; Gaps 3;

QY 26 KLAIVAKKSGDDRNQFHRRFALLQGTGSPFSELLPDMGTNCTGDLVDLIONEP 85
DB 173 RVHFTKAPIDMTTSQYLEWVASDLDLSKA-TAEILLDVAIANNQVPLVK-ESTNQF 230
QY 86 PAPAS-LILPDVAP 98
DB 231 HAYNDMLFPAP 244

RESULT 11
A82839
hypothetical protein XF0172 [imported] - Xylella fastidiosa (strain 985C)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: A82839
R/anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequet
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: A82839

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-598 <STM>
A/Cross-references: UNIPROT:Q9PGX6; GB:AE003871; GB:AE003849; NID:g9104966; PIDN:AAF8298
A/Experimental source: strain 985C
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briano, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carver, H
as-Neto, E.; Docena, C.; El-Dorty, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm
J.D.; Ungerleider, M.L.; Kempner, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
M.; Tanaka, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A/Reference number: A59328
A/Contents: annotation
C/Genetics:
A/Gene: XF0172

Query Match 12.8%; Score 66; DB 2; Length 598;
Best Local Similarity 31.0%; Pred. No. 26;
Matches 22; Conservative 8; Mismatches 31; Indels 10; Gaps 3;

QY 22 EGMKLAIVAKKPSG--DNRVQFHRRFALLQGTGSPFSELLPDMG--TTNCTVGDV 77
DB 442 EGMGIVASLSGKELGYDVAIVF-----GYLDALSPAIRLVVDYTGHTGKWTACV 495
QY 78 DLLIONEPFAP 88
DB 496 DYIVENSATSP 506

RESULT 12
G71804
translational elongation factor EF-Ts - Helicobacter pylori (strain J99)
C/Species: Helicobacter pylori
A/Variety: strain J99

C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C/Accession: G71804
R/Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Voris, G.F.;
Nature 397, 176-180, 1999
A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A/Reference number: A71800; MUID:99120557; PMID:9923682
A/Accession: G71804

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-355 <ARN>
A/Cross-references: UNIPROT:Q9ZJ71; GB:AE001567; GB:AE001439; NID:g4156065; PIDN:AAD0702
A/Experimental source: strain J99
C/Genetics:
A/Gene: ttf
C/Superfamily: translation elongation factor EF-Ts

Query Match 12.6%; Score 65; DB 2; Length 355;
Best Local Similarity 22.9%; Pred. No. 18;
Matches 24; Conservative 17; Mismatches 34; Indels 30; Gaps 3;

QY 11 IRLSDPDPQSGWKLAIVAKKPSGDDRNQFHI-----RRFALLQGTG---- 55
DB 78 INSEDFVAKNGKFKEL--VKETLETIKTHNIHTEELKSPIDNKPFEELHSQLAVI 134
QY 56 -----KSPFSELLPDMGTNCTGDLVDLIONEPFAP 88
DB 135 GENIIVRKIAHAKPSSHTINGYAHSNKRVGLTAEYNEKNAP 179

RESULT 13
D95952
probable glycosyltransferase, forming alpha glycosyl linkages protein exp7 [imported] -
C/Species: Sinorhizobium meliloti
C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C/Accession: D95952
R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A/Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A/Reference number: A95842; MUID:21396508; PMID:11481431
A/Accession: D95952
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-440 <KUN>
A/Cross-references: UNIPROT:Q92V35; GB:AL591985; PIDN:CAC49284.1; PID:g15140770; GSPDB:G
A/Experimental source: strain 1021, megaplasmid pSymB
R/Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kies, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A/Reference number: A96039; MUID:21368234; PMID:11474104
A/Contents: annotation
C/Genetics:
A/Gene: exp7; SMD21308
A/Genome: plasmid

Query Match 12.6%; Score 65; DB 2; Length 440;
Best Local Similarity 28.6%; Pred. No. 23;
Matches 14; Conservative 10; Mismatches 25; Indels 0; Gaps 0;

QY 10 LIRRLSDPDPQSGWKLAIVAKKPSGDDRNQFHIHRFALLQGTGSP 58
DB 378 LADRLSDVAVKPEAMDRHLHATLRPTGHSARAHADYLRLLKXRRSP 426

RESULT 14
JC7906
sucrose 1F-fructosyltransferase (BC 2.4.1.99) - wheat
N/Alternate names: 1-SST; fructosyltransferase 2; Wf2 protein
C/Species: Triticum aestivum (common wheat)

C:Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 09-Jul-2004
C:Accession: JCT9906
R:Kawakami, A., Yoshida, M.
BioSci. Molechnol. Biochem. 66, 2297-2305, 2002
A:Title: Molecular characterization of sucrose 1-fructosyltransferase and sucrose
A:Reference number: JCT9905; PMID:22394650; PMID:12506954
A:Accession: JCT9906
A:Molecule type: mRNA
A:Residues: 1-662 <KAM>
A:Cross-references: UNIPROT:O8W430; DDBJ:AB029988
C:Comment: This enzyme, which is a vacuole-type fructosyltransferase and a fructan-biosynthesizing enzyme, transfers a fructosyl moiety from one sucrose to another, resulting in the formation of trisaccharides.
C:Genetics:
A:Gene: wfc2
C:Keywords: glycosyltransferase; hexosyltransferase

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 10, 2005, 23:08:19 ; Search time 193 Seconds

(without alignments)
292.159 Million cell updates/sec

Title: US-10-001-254-6

Perfect score: 517

Sequence: 1 TTYRCLNVGLIRKLSDFIDP.....LLIQNEFPAPASLLLPDPAVP 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	517	100.0	460	1 IRA4_HUMAN	Q9NWZ3 homo sapien
2	513	99.2	218	2 Q7Z6A7	Q7Z6A7 homo sapien
3	513	99.2	292	2 Q7Z6A8	Q7Z6A8 homo sapien
4	476	92.1	197	2 Q9D250	Q9D250 mus musculu
5	476	92.1	459	1 IRA4_MOUSE	Q814K2 mus musculu
6	287	55.5	382	2 Q7ZVW7	Q7ZVW7 brachydanio
7	287	55.5	483	2 Q6IWL3	Q6IWL3 brachydanio
8	287	55.5	609	2 AAT37635	AAT37635 brachydanio
9	98.5	19.1	609	2 Q8C7U8	Q8C7U8 mus musculu
10	98.5	19.1	609	2 Q8C840	Q8C840 mus musculu
11	96.5	18.7	596	2 Q9Y616	Q9Y616 homo sapien
12	96.5	18.7	596	2 AAH57800	AAH57800 homo sapi
13	96.5	18.7	596	2 AAH69388	AAH69388 homo sapi
14	95	18.4	609	2 Q8K482	Q8K482 mus musculu
15	88	17.0	296	2 Q6Y151	Q6Y151 rattus norv
16	88	17.0	296	2 AAQ91937	AAQ91937 rattus norv
17	86	16.6	672	2 Q7ZYEA	Q7ZYEA xenopus lae
18	82	15.9	162	1 Q8C1X0	Q8C1X0 mus musculu
19	82	15.9	296	1 MYR8_MOUSE	P23366 mus musculu
20	79	15.3	590	1 IRA2_HUMAN	O34187 homo sapien
21	75.5	14.6	257	2 Q347Z4	Q347Z4 bacillus su
22	74.5	14.4	550	2 Q9D150	Q9D150 mus musculu
23	74.5	14.4	550	2 Q8VC10	Q8VC10 mus musculu
24	73.5	14.2	539	2 Q6PB60	Q6PB60 mus musculu
25	73.5	14.2	539	2 AAH59871	AAH59871 mus muscu
26	72.5	14.0	824	1 MLT1_HUMAN	Q9UDY8 homo sapien
27	72	13.9	462	1 TUBE_DROME	P22812 drosophila
28	71.5	13.8	562	1 Q8DMT6	Q8DMT6 synecococc
29	71.5	13.8	1076	1 HSER_CAVPO	P70106 cavia porce
30	71.5	13.8	5826	2 Q76KY0	Q76KY0 streptomyce
31	71.5	13.8	5826	2 BAD08373	BAD08373 streptomy

32	71	13.7	259	1 APA1_RAT	P04639 rattus norv
33	71	13.7	1411	2 Q6FSJ5	Q6FSJ5 candida gla
34	70.5	13.6	151	2 Q8CC82	Q8CC82 mus musculu
35	70.5	13.6	565	2 Q88RV5	Q88RV5 pseudomonas
36	70.5	13.6	574	2 Q6YBS0	Q6YBS0 mus musculu
37	70.5	13.6	574	2 Q8C5W0	Q8C5W0 mus musculu
38	70.5	13.6	574	2 AAQ24762	AAQ24762 mus muscu
39	70.5	13.6	622	2 Q6YBS1	Q6YBS1 mus musculu
40	70.5	13.6	622	2 Q8CEA0	Q8CEA0 mus musculu
41	70.5	13.6	622	2 Q8CFP1	Q8CFP1 mus musculu
42	70.5	13.6	622	2 AAQ24761	AAQ24761 mus muscu
43	70	13.5	1144	2 Q7PM73	Q7PM73 anopheles g
44	69.5	13.4	413	2 Q6JEK7	Q6JEK7 dasypus nov
45	69.5	13.4	413	2 AA875798	AA875798 dasypus n

ALIGNMENTS

RESULT 1	IRAK4_HUMAN	STANDARD	PRT	460 AA.
AC	Q9NWZ3; Q8TDF7; Q9Y589;			
DT	01-OCT-2004 (Rel. 45, Created)			
DT	01-OCT-2004 (Rel. 45, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Interleukin-1 receptor-associated kinase-4 (EC 2.7.1.-) (IRAK-4) (NY-REN-64 antigen).			
GN	Name=IRAK4;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	SEQUENCE FROM N.A., FUNCTION, AND INTERACTIONS WITH IRAK1 AND TRAF6.			
RP	MEDLINE=21957277; PubMed=11960013; DOI=10.1073/pnas.082100399;			
RA	Li S., Strelow A., Fontana E.J., Wesche H.;			
RT	"IRAK4: A novel member of the IRAK family with the properties of an			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:5567-5572(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99438124; PubMed=10508479;			
RA	Scanlan M.J., Gordon J.D., Williamson B., Stockert E., Bander N.H.,			
RA	Jongeneel C.V., Gure A.O., Jager D., Jager E., Knuth A., Chen Y.-T.,			
RA	Old L.J.;			
RT	"Antigens recognized by autologous antibody in patients with renal-			
RL	cell carcinoma."			
RN	Int. J. Cancer 83:456-464(1999).			
RP	[3]			
RX	SEQUENCE FROM N.A.			
RA	Pubmed=14702039; DOI=10.1038/ng1285;			
RA	Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,			
RA	Wakamatsu K., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,			
RA	Sekine M., Ohtayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,			
RA	Yamanoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,			
RA	Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,			
RA	Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,			
RA	Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,			
RA	Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa K.,			
RA	Yamazaki M., Niinomiya K., Ishibashi T., Yamashita H., Murakawa K.,			
RA	Fujimori Y., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,			
RA	Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Horita T.,			
RA	Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,			
RA	Imomae N., Mutsaers K., Komai F., Hara R., Takeuchi K., Arita M.,			
RA	Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,			
RA	Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,			
RA	Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,			
RA	Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,			
RA	Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,			
RA	Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujisawa T.,			
RA	Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y.,			

RA Kawabata A., Hikiiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Moritaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isegai T., Sugano S.,
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RT Nat. Genet. 36:40-45(2004).
 RL [4]
 RN
 RP SEQUENCE FROM N.A., AND VARIANTS ARG-98; ARG-390 AND THR-428.
 RA Rieder M.J., Arnel T.Z., Carrington D.P., Ouna M., Kuldane S.A.,
 RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.,
 RT "SeattleSNPs: NHGRI HL66682 program for genomic applications, UW-
 RT FHRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RL Submitted (NCV-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Mansina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshtayuk S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Vallaloon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shvachenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Schein J.E., Jones S.J.M., Marra M.A.,
 RA Schnerch A., Scher J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC
 CC -1- FUNCTION: Involved in IL1R-induced NF-kappa-B (NFKB) activation as
 CC well as the activation of mitogen-activated protein (MAP) kinase
 CC pathways. Phosphorylates IRAK1.
 CC
 CC -1- SUBUNIT: Interacts with TRAF6 and IRAK1.
 CC
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. Pelle
 CC subfamily.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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 CC
 CC -----
 CC EMBL AF445802; AAM15772.1; -;
 CC EMBL AF155118; AAD42884.1; -;
 CC EMBL AK000528; BAA91232.1; -;
 CC EMBL AY186092; AAH5440.1; -;
 CC EMBL BC013316; AAH13316.1; -;
 CC HSSP; Q62838; ILUP.
 CC
 CC GeneW; HGNC:17967; IRAK4.
 CC
 CC MIM; 606883; -;
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR001245; Tyr_kinase.
 CC Pfam; PF00069; Pkinase; 1.
 CC PRINTS; PR00109; TYRKINASE.
 CC PRODOM; PD000001; Prot_kinase; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 CC PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
 CC ATP-binding; Polymorphism; Serine/threonine-protein kinase;

KW Transferase.
 FT 186 454 Protein kinase.
 FT NP_BIND 192 200 ATP (By similarity).
 FT BINDING 213 213 ATP (By similarity).
 FT ACT_SITE 311 311 Proton acceptor (By similarity).
 FT VARIANT 98 98 S -> R.
 FT VARIANT 390 390 /FTID=VAR_019354.
 FT VARIANT 428 428 H -> R.
 FT VARIANT 428 428 /FTID=VAR_019355.
 FT CONFLICT 81 81 A -> T.
 FT CONFLICT 432 432 V -> A (in Ref. 1).
 FT CONFLICT 437 437 L -> R (in Ref. 2).
 FT CONFLICT 444 444 R -> S (in Ref. 2).
 FT CONFLICT 451 451 Q -> H (in Ref. 2).
 SQ SEQUENCE 460 AA; 51529 MW; 6C8156ADP25FP81E CRC64;
 Query Match 100.0%; Score 517; DB 1; Length 460;
 Best Local Similarity 99.0%; Pred. No. 1,4e-49;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TYVRCINVLIRKLSDFIDPQEGWKLAVALIKKSGDDRYNQFHIRRFEALLQTKGSPTS 60
 DB 9 TYVRCINVLIRKLSDFIDPQEGWKLAVALIKKSGDDRYNQFHIRRFEALLQTKGSPTS 68
 QY 61 ELTFDMGTNCVGLVDLILQNEFFAPASLLDPAVP 98
 DB 69 ELTFDMGTNCVGLVDLILQNEFFAPASLLDPAVP 106
 RESULT 2
 Q726A7 PRELIMINARY; PRT; 218 AA.
 AC Q726A7;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin-1 receptor associated kinase 4 mutant form 2.
 GN Name=IRAK4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Medvedev A.B., Lentschat A., Kuhns D.B., Bianco J.C.G., Salkowski C.,
 RA Zhang S., Arditi M., Gallin J.I., Vogel S.N.,
 RT "Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to
 RT Lipopolysaccharide and Interleukin-1 in a Patient with Recurrent
 RT Bacterial Infections.";
 RT J. Exp. Med. 0:0-0(2003).
 DR EMBL AY283671; AAP57090.1; -;
 DR GO; GO:0016301; P-kinase activity; IEA.
 DR GO; GO:0004872; F-receptor activity; IEA.
 KW Kinase; Receptor.
 SQ SEQUENCE 218 AA; 24257 MW; B42D2896DACBDF9 CRC64;
 Query Match 99.2%; Score 513; DB 2; Length 218;
 Best Local Similarity 99.0%; Pred. No. 1.6e-49;
 Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TYVRCINVLIRKLSDFIDPQEGWKLAVALIKKSGDDRYNQFHIRRFEALLQTKGSPTS 60
 DB 9 TYVRCINVLIRKLSDFIDPQEGWKLAVALIKKSGDDRYNQFHIRRFEALLQTKGSPTS 68
 QY 61 ELTFDMGTNCVGLVDLILQNEFFAPASLLDPAVP 98
 DB 69 ELTFDMGTNCVGLVDLILQNEFFAPASLLDPAVP 106
 RESULT 3
 Q726A8

ID Q726A8 PRELIMINARY; PRT; 292 AA.
AC Q726A8
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Interleukin-1 receptor associated kinase 4 mutant form 1.
GN Name=IRAK4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Medvedev A.E., Lentschat A., Kuhns D.B., Blanco J.C.G., Salkowski C.,
Zhang S., Altieri M., Gallin J.I., Vogel S.N.;
RT "Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to
Lipopolysaccharide and Interleukin-1 in a Patient with Recurrent
Bacterial Infections";
RL J. Exp. Med. 0:0-0(2003).
DR EMBL; AY283670; AAP57089.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00069; Kinase_1.
DR PRODOM; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Kinase; Receptor.
SQ SEQUENCE 292 AA; 32704 MW; 58F1708A63BD3BES CRC64;

Query Match 99.2%; Score 513; DB 2; Length 292;
Best Local Similarity 99.0%; Pred. No. 2.3e-49;
Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TYVCLNGLIRKISDFIDPQGWKLAIVAKKSGDRYNOFIRFEALLQTKSPPTS 60
DB 9 TYVCLNGLIRKISDFIDPQGWKLAIVAKKSGDRYNOFIRFEALLQTKSPPTS 68
QY 61 ELFPDGTCTGVDLVLLIQNEFPAPASILLPDVAP 98
DB 69 ELFPDGTCTGVDLVLLIQNEFPAPASILLPDVAP 106

RESULT 4
Q9D250 PRELIMINARY; PRT; 197 AA.
AC Q9D250;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched
library, clone:9330209D03 product:interleukin-1 receptor-associated
kinase 4.
GN Name=Irak4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection";

RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RA The PANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,
Suni M., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kaishwagi K.,
Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arahata T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuo M.,
Hasegaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK020397; BAB32090.2; -.
DR MGD; MGI:2182474; Irak4.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR01029; DEATH_1like.
DR InterPro; IPR01029; DEATH_1like.
DR Pfam; PF00531; Death_1.
KW Kinase; Receptor.
SQ SEQUENCE 197 AA; 21695 MW; 142B61EB8A614898 CRC64;

Query Match 92.1%; Score 476; DB 2; Length 197;
Best Local Similarity 90.8%; Pred. No. 2.2e-45;
Matches 89; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 TYVCLNGLIRKISDFIDPQGWKLAIVAKKSGDRYNOFIRFEALLQTKSPPTS 60
DB 9 TYVCLNGLIRKISDFIDPQGWKLAIVAKKSGDRYNOFIRFEALLQTKSPPTS 68
QY 61 ELFPDGTCTGVDLVLLIQNEFPAPASILLPDVAP 98
DB 69 ELFPDGTCTGVDLVLLIQNEFPAPASILLPDVAP 106

RESULT 5
IRAK4_MOUSE

1D IRRA4_MOUSE STANDARD; PRT: 459 AA.
2D OBR4K2; O80WMI;
3D 01-OCT-2004 (Rel. 45, Created)
4D 01-OCT-2004 (Rel. 45, Last sequence update)
5D 01-OCT-2004 (Rel. 45, Last annotation update)
6D Interleukin-1 receptor-associated kinase-4 (EC 2.7.1.-) (IRAK-4),
7D GN=Irak4;
8D OS Mus musculus (Mouse).
9D Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
10D OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
11D NCBI_Taxid=10090;
12D
13D
14D
15D
16D
17D
18D
19D
20D
21D
22D
23D
24D
25D
26D
27D
28D
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119D
120D
121D
122D
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RT Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Involved in IL1R-induced NF-kappa-B (NFKB) activation as
CC well as the activation of mitogen-activated protein (MAP) kinase
CC pathways. Phosphorylates IRAK1 (By similarity).
CC -1- SUBUNIT: Interacts with TRAF6 and IRAK1 (By similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. Pelle
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, AF445803; AAM15773.1; -.
CC EMBL, AK028837; BAC26146.1; -.
CC EMBL, BC051676; AAHS1676.1; -.
CC HSSP, P36897; 11AS.
CC MGD: MG1:2182474; Irak4.
CC InterPro: IPR000488; Death.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR001245; Tyr_kinase.
CC Pfam, PF00531; Death; 1.
CC Pfam, PF00069; Pkinase; 1.
CC PRINTS: PR00109; TYRKINASE
CC ProDom: PD000001; Prot_kinase; 1.
CC PROSITE, PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE, PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE, PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
CC ATP-binding; Serine/threonine-protein kinase; Transferase.
CC DOMAIN 186 454 Protein kinase.
CC FT NP_BIND 192 200 ATP (By similarity).
CC FT BINDING 213 213 ATP (By similarity).
CC FT ACT_SITE 311 311 Proton acceptor (By similarity).
CC FT CONFLICT 321 321 K -> R (in Ref. 3).
CC SQ SEQUENCE 459 AA; 50871 MW; FCL1AD06983B7AEB CRC64;

Query Match 92.1%; Score 476; DB 1; Length 459;
Best Local Similarity 90.8%; Pred. No. 6e-45;
Matches 89; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 TYVRLANVGLIRKLSDFIDPQEGWKKLAVALIKKPSGDDRYNQPHIRFEALQTKSPFS 60
Db 9 TYIRINLVGILIKRLSDFIDPQEGWKKLAVALIKKPSGDDRYNQPHIRFALLQTKSPFC 68

QY 61 ELLFDGNTTCVGDVLDLILQNEERPAASILLPDANP 98
Db 69 ELLFDGNTTCVGDVLDVLIQIELEPAATILLPDAPP 106

RESULT 6
Q7ZVM7 PRELIMINARY; PRT; 382 AA.
AC Q7ZVM7;
DT 01-JUN-2003 (TEMBLrel. 24, Created)
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DN Similar to interleukin-1 receptor-associated kinase 4.
DS Name=gzc:55553;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=AB; Tissue=whole body;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan A., Moore T., Max S.I., Wang J., Hasteh F.,
RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stappleton M., Soares M.B., Bonaldo M.F., Cavaletto T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalske U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maiz M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=whole body;
RA Strausberg K.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045381; AA045381.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR01029; DEATH_like.
DR InterPro; IPR01029; Kinase_like.
DR InterPro; IPR00719; Prot_kinase.
DR Pfam; PF00531; Death_1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
KM ATP-binding; Kinase; Receptor.
SQ SEQUENCE 382 AA; 41769 MW; 2FDFDB572B4CB2B CRC64;

Query Match 55.5%; Score 287; DB 2; Length 382;
Best Local Similarity 53.7%; Pred. No. 1.4e-23;
Matches 51; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

QY 1 TVVRCIANVGLIRKLSDFIDPOEGWKLAVALIKKPSGDDRYNQFHIRREALLQTKSPTS 60
DB 8 TPVKRLRYSAIRALADLDPQDTWRSIMADISRCGEPRTYQMHRRREACVLOGKSPTM 67
QY 61 ELFPDWGTTNCTVGDVLDLIONEFPAPASILLPD 95
DB 68 ELFPDWGTSCTVGDVLEILRHQLFAAVTVLLPD 102

RESULT 7
O61WL3 PRELIMINARY; PRT; 483 AA.
AC O61WL3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Interleukin-1 receptor-associated kinase 4.
GN Name=Itak4;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Phelan P.E., III, Mellon M.T., Kim C.H.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY616584; AAT37635.1; -.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000488; Death_1like.
DR InterPro; IPR01029; Kinase_like.
DR InterPro; IPR01029; DEATH_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00531; Death_1.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
KM ATP-binding; Kinase; Receptor.
SQ SEQUENCE 483 AA; 53708 MW; 5F0BDBAC250561F7 CRC64;

Query Match 55.5%; Score 287; DB 2; Length 483;
Best Local Similarity 53.7%; Pred. No. 1.4e-23;
Matches 51; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

QY 1 TVVRCIANVGLIRKLSDFIDPOEGWKLAVALIKKPSGDDRYNQFHIRREALLQTKSPTS 60
DB 8 TPVKRLRYSAIRALADLDPQDTWRSIMADISRCGEPRTYQMHRRREACVLOGKSPTM 67
QY 61 ELFPDWGTTNCTVGDVLDLIONEFPAPASILLPD 95
DB 68 ELFPDWGTSCTVGDVLEILRHQLFAAVTVLLPD 102

RESULT 8
AAT37635 PRELIMINARY; PRT; 483 AA.
AC AAT37635;
DT 01-JUN-2004 (TREMBlrel. 27, Created)
DT 01-JUN-2004 (TREMBlrel. 27, Last sequence update)
DT 01-JUN-2004 (TREMBlrel. 27, Last annotation update)
DE Interleukin-1 receptor-associated kinase 4.
GN IRAK4.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Phelan P.E., III, Mellon M.T., Kim C.H.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY616584; AAT37635.1; -.
KM Kinase; Receptor.
SQ SEQUENCE 483 AA; 53708 MW; 5F0BDBAC250561F7 CRC64;

Query Match 55.5%; Score 287; DB 2; Length 483;
Best Local Similarity 53.7%; Pred. No. 1.4e-23;
Matches 51; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

QY 1 TVVRCIANVGLIRKLSDFIDPOEGWKLAVALIKKPSGDDRYNQFHIRREALLQTKSPTS 60
DB 8 TPVKRLRYSAIRALADLDPQDTWRSIMADISRCGEPRTYQMHRRREACVLOGKSPTM 67
QY 61 ELFPDWGTTNCTVGDVLDLIONEFPAPASILLPD 95
DB 68 ELFPDWGTSCTVGDVLEILRHQLFAAVTVLLPD 102

RESULT 9
O8CTU8 PRELIMINARY; PRT; 609 AA.
AC O8CTU8;
DT 08CTU8;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
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DT 01-MAR-2003 (TREMblrel. 23, Created)
 DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 25, Last annotation update)
 DE Mus musculus ES cells cDNA, RIKEN full-length enriched library,
 DE clone: C330013G03 product: similar to interleukin-1 receptor-associated
 DE kinase M, full insert sequence.
 GN Name=Irak3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RN R1
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=9279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.",
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RN R2
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 [3]
 RN R3
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA The FANTOM Consortium,
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.",
 RL Nature 420:563-573(2002).
 [4]
 RN R4
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.",
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RN R5
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.",
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RN R6
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK049210; BAC33612.1; -.
 DR MGI; MGI:1921164; Irak3.

DR GO: GO:0016301; P:kinase activity; IDA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IDA.
 DR GO: GO:0007165; P:signal transduction; IDA.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR011029; DEATH_like.
 DR InterPro: IPR011009; Kinase_like.
 DR InterPro: IPR000719; Prot_kinase.
 DR Pfam: PF00531; Death_1.
 DR Pfam: PF00069; Kinase_1.
 DR Prodom: PD000001; Prot_kinase.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Kinase; Receptor.
 SQ SEQUENCE 609 AA; 69425 MW; C8FB51065B2313C4 CRC64;
 Query Match 19.1%; Score 98.5; DB 2; Length 609;
 Best Local Similarity 31.5%; Pred. No. 0.036;
 Matches 23; Conservative 13; Mismatches 30; Indels 7; Gaps 1;
 QY 8 VGLIRLSDPFIPOEGMKLAVAIKKPGDDRYNOFHIRRFEALLQNGKSPSTSLPDWG 67
 Db 25 LSELGCIIDSCDGLPGLMGLARLSN-----SWDVRIHEKYVNGKSGTRELMSWA 77
 QY 68 TTNCIVGDIIVDL 80
 Db 78 QKNKITGIDLEVL 90
 RESULT 10
 ID Q8CE40 PRELIMINARY; PRT; 609 AA.
 AC Q8CE40; Q8K1S8;
 DT 01-MAR-2003 (TREMblrel. 23, Created)
 DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
 DT 01-OCT-2004 (TREMblrel. 28, Last annotation update)
 DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
 DE library, clone: 473246H23 product: similar to interleukin-1 receptor-
 DE associated kinase M, full insert sequence (IL-1 receptor-associated
 DE kinase M).
 GN Name=Irak3; Synonyms=Irak-M;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RN R1
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=9279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.",
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RN R2
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 [3]
 RN R3
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RA The FANTOM Consortium,
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.",
 RL Nature 420:563-573(2002).
 [4]
 RN R4
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.",
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RN R5
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.",
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RN R6
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK049210; BAC33612.1; -.
 DR MGI; MGI:1921164; Irak3.

RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=20530913; PubMed=11076861.
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RL sequencing pipeline with 384 multicapillary sequencer.";
 RN Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito K., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunuki A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=balb/c;
 RX MEDLINE=22050158; PubMed=12054681;
 RA Rosati O., Martin M.U.,
 RT "Cloning of murine IL-1 receptor-associated-kinase M.";
 RL Biochem. Biophys. Res. Commun. 293:1472-1477(2002).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=balb/c;
 RA Rosati O.,
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK029057; BAC26270.1; -
 DR EMBL; AJ440757; CAD29448.2; -
 DR MGI:1921164; Irak3.
 KW Kinase; Receptor.
 SQ SEQUENCE 609 AA; 68455 MW; A63E010C9F29D856 CRC64;
 Query Match 19.1%; Score 98.5; DB 2; Length 609;
 Best Local Similarity 31.5%; Pred. No. 0.036;
 Matches 23; Conservative 13; Mismatches 30; Indels 7; Gaps 1;
 QY 8 VGLIRKLSDFIDPQEGWKLVAIKKSGDRNQFHIRFALLQTKSPSTSLFDWG 67
 Db 25 LGEICGLIDSCDGLGWRGLAERLSN-----SWLDVRHIEKYVQCKSGTRELMSWA 77
 QY 68 TTNCTVGDVLDL 80
 Db 78 QKNTKIDGLLEVL 90
 RESULT 11
 QY616 PRELIMINARY; PRT; 596 AA.
 AC QY616;
 DT 01-NOV-1999 (TIREMBLrel. 12; Created)
 DT 01-NOV-1999 (TIREMBLrel. 12; Last sequence update)
 DT 01-OCT-2004 (TIREMBLrel. 28; Last annotation update)
 DE IL-1 receptor-associated-kinase-M (interleukin-1 receptor-associated
 kinase 3).
 GN Name=IRAK3;
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99315891; PubMed=10383454;
 RX Weesche H., Gao X., Li X., Kirschning C.J., Stark G.R., Cao Z.,
 RT "IRAK-M is a novel member of the Pelle/interleukin-1 receptor-
 RT associated kinase (IRAK) family.";
 RL J. Biol. Chem. 274:19403-19410(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones; and Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Bata S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Straubeberg R.,
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RA Straubeberg R.,
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF113136; AAD40879.1; -
 DR EMBL; BC057800; AAH57800.1; -
 DR EMBL; BC069388; AAH59388.1; -
 DR GeneW; HGNC:17020; IRAK3.
 DR GO; GO:0004672; F:protein kinase activity; TKS.
 DR GO; GO:0004702; F:receptor signaling protein serine/threonine...; TKS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu...; TKS.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; TKS.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH like.
 DR InterPro; IPR011009; kinase like.
 DR InterPro; IPR000719; Prot_kinase.
 DR Pfam; PF00531; Death_1.
 DR Pfam; PF00063; Kinase_1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS50017; DEATH DOMAIN; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Kinase; Receptor.
 SQ SEQUENCE 596 AA; 67752 MW; E37433EAD07E38BE CRC64;
 Query Match 18.7%; Score 96.5; DB 2; Length 596;
 Best Local Similarity 31.5%; Pred. No. 0.058;
 Matches 23; Conservative 12; Mismatches 31; Indels 7; Gaps 1;
 QY 8 VGLIRKLSDFIDPQEGWKLVAIKKSGDRNQFHIRFALLQTKSPSTSLFDWG 67
 Db 25 LGEICAVLIDSCDGLGWRGLAERLSN-----SWLDVRHIEKYVQCKSGTRELMSWA 77
 QY 68 TTNCTVGDVLDL 80

Db 78 QKNKTTGDLQVL 90

RESULT 12

AAH57800 PRELIMINARY; PRT; 596 AA.
 AC AAH57800; ID
 DT 02-MAR-2004 (TREMblrel. 27, Created)
 DT 02-MAR-2004 (TREMblrel. 27, Last sequence update)
 DE Interleukin-1 receptor-associated kinase 3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S., Krzywinski M.I., Skalka U., Smalls D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC057800; AAH57800.1; -.
 KW kinase; Receptor.
 SQ SEQUENCE 596 AA; 67752 MW; E37433EADD7E38BE CRC64;

Query Match 18.7%; Score 96.5; DB 2; Length 596;
 Best Local Similarity 31.5%; Pred. No. 0.058; Indels 7; Gaps 1;
 Matches 23; Conservative 12; Mismatches 31;
 QY 8 VGLIRKLSDFIDPQEGWKKLVAIKKPSGDDRYNQFHRRFALLQTKGKPTSLFDWG 67
 DB 25 LGEICAVLDSGCGALGWRGLAERLSS-----SWLDVRHIEKYVDGKSGTRELMSWA 77
 QY 68 TTNCTVGDIVDLL 80
 DB 78 QKNKTTGDLQVL 90

RESULT 13

AAH69388 PRELIMINARY; PRT; 596 AA.
 AC AAH69388; ID
 DT 20-MAY-2004 (TREMblrel. 27, Created)
 DT 20-MAY-2004 (TREMblrel. 27, Last sequence update)
 DE Interleukin-1 receptor-associated kinase 3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S., Krzywinski M.I., Skalka U., Smalls D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RA Strausberg R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC069388; AAH69388.1; -.
 KW kinase; Receptor.
 SQ SEQUENCE 596 AA; 67752 MW; E37433EADD7E38BE CRC64;

Query Match 18.7%; Score 96.5; DB 2; Length 596;
 Best Local Similarity 31.5%; Pred. No. 0.058; Indels 7; Gaps 1;
 Matches 23; Conservative 12; Mismatches 31;
 QY 8 VGLIRKLSDFIDPQEGWKKLVAIKKPSGDDRYNQFHRRFALLQTKGKPTSLFDWG 67
 DB 25 LGEICAVLDSGCGALGWRGLAERLSS-----SWLDVRHIEKYVDGKSGTRELMSWA 77
 QY 68 TTNCTVGDIVDLL 80
 DB 78 QKNKTTGDLQVL 90

RESULT 14

Q8K4B2 PRELIMINARY; PRT; 609 AA.
 AC Q8K4B2; ID
 DT 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
 DE Interleukin-1 receptor-associated kinase M.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=22145925; PubMed=12150927;
 RA Kobayashi K., Hernandez L.D., Galan J.E., Janeway C.A. Jr., Medzhitov R., Flavell R.A.;
 RL Cell 110:191-202(2002).
 DR MGD; MGI:1921164; Irak3.
 GO; GO:0016301; P:kinase activity; IRA.
 GO; GO:0006468; P:protein amino acid phosphorylation; IRA.

DR GO:0007165; P:signal transduction; IDA.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR011009; Kinase_like.
 DR InterPro; IPR000719; Prot_Kinase.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00069; Kinase; 1.
 DR ProDom; PD000001; Prot_Kinase; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Kinase; Receptor.
 SQ SEQUENCE 609 AA; 68657 MW; 19BAD129F854DD73 CRC64;

Query Match 18.4%; Score 95; DB 2; Length 609;
 Best Local Similarity 32.4%; Pred. No. 0.089;
 Matches 24; Conservative 12; Mismatches 28; Indels 10; Gaps 2;

QY 10 LIRKLSDFIDPQ--GKKLAIVAIKKPSGDDRYNQPHIRFEALLQTGKSPTELLFDW 66
 DB 24 LIGELCGILDSWDGPIGWWGLAERLSN-----SWLDVRIIEKYKNGKSGTRELLEMSW 76
 QY 67 GTTNCYGVGLVDLL 80
 DB 77 AQKKNKTIGDLLEVL 90

RESULT 15

OCY1S1 PRELIMINARY; PRT; 296 AA.
 AC OCY1S1;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Myeloid differentiation primary response gene 88.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Miscar; TISSUE=Spleen;
 RA Li Y., Ji A., Schaffer M.K.;
 RL EMBL; AY191270; AAC91937.1; -.
 DR EMBL; AY191270; AAC91937.1; -.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR00157; TIR.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF01582; TIR; 1.
 DR Pfam; PF00069; Kinase; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50104; TIR; 1.
 DR SEQUENCE 296 AA; 33883 MW; 7A74304BE61DBC80 CRC64;

Query Match 17.0%; Score 88; DB 2; Length 296;
 Best Local Similarity 35.0%; Pred. No. 0.23;
 Matches 28; Conservative 11; Mismatches 25; Indels 16; Gaps 4;

QY 6 LNVGLIRKLSDFIDPQ---EGWKLAIVAIKKPSGDDRYNQPHIRFEALLQTGKSPTE 61
 DB 25 LNVGVRRRLSLFLNPRTTAAADWTSLEEM-----GFEYLEIRFE---TRPDPTRS 73
 QY 62 LLEFDW-GTTNCTGVGLVDLL 80
 DB 74 LLDAMQGRSGSSVGRLLLELL 93

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OM protein - protein search, using sw model

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Total number of hits satisfying chosen parameters: 478139

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Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517	100.0	206	4	US-09-166-350-21
2	96.5	18.7	596	3	US-09-135-232-2
3	96.5	18.7	596	4	US-09-863-549-2
4	79	15.3	590	2	US-08-980-060-2
5	79	15.3	590	3	US-08-980-060-2
6	79	15.3	590	4	US-09-307-185-2
7	79	15.3	625	2	US-08-980-060-4
8	79	15.3	625	3	US-09-307-185-4
9	79	15.3	625	4	US-09-773-753-4
10	69.5	13.4	398	4	US-09-360-545-20
11	69.5	13.4	593	3	US-09-234-393-24
12	69.5	13.4	593	3	US-09-234-393-50
13	69.5	13.4	593	3	US-09-234-393-52
14	69.5	13.4	593	3	US-09-234-393-54
15	69.5	13.4	593	4	US-09-865-171-24
16	69.5	13.4	593	4	US-09-865-171-50
17	69.5	13.4	593	4	US-09-865-171-52
18	69.5	13.4	593	4	US-09-865-171-54
19	69.5	13.4	593	4	US-09-398-395A-50
20	69.5	13.4	593	4	US-09-887-586A-50
21	69.5	13.4	593	4	US-09-895-752-50
22	69.5	13.4	593	4	US-09-903-012B-50
23	69.5	13.4	593	4	US-09-900-797-50
24	66.5	12.9	215	4	US-09-489-039A-12848
25	66	12.8	70	4	US-09-248-796A-21148
26	66	12.8	328	4	US-09-252-991A-27822
27	64.5	12.5	506	3	US-09-134-001C-3307

28	64.5	12.5	662	4	US-09-534-228B-2	Sequence 2, Appli
29	63.5	12.3	501	2	US-08-980-060-6	Sequence 6, Appli
30	63.5	12.3	501	3	US-09-307-185-6	Sequence 6, Appli
31	63.5	12.3	501	4	US-09-773-753-6	Sequence 6, Appli
32	63	12.2	430	4	US-09-489-039A-7580	Sequence 7580, Ap
33	62.5	12.1	125	4	US-09-543-681A-7171	Sequence 7171, Ap
34	62.5	12.1	499	4	US-09-543-681A-6427	Sequence 6427, Ap
35	62.5	12.1	520	4	US-09-724-623-124	Sequence 124, App
36	62.5	12.1	680	4	US-09-248-796A-16453	Sequence 16453, A
37	62.5	12.1	1423	3	US-08-810-712-10	Sequence 10, Appl
38	62.5	12.1	1431	4	US-09-538-092-1198	Sequence 1198, Ap
39	62.5	12.1	1674	2	US-08-968-542C-12	Sequence 12, Appl
40	62.5	12.1	1674	4	US-09-554-467A-12	Sequence 12, Appl
41	62	12.0	428	3	US-09-608-285A-7	Sequence 7, Appli
42	62	12.0	428	3	US-09-350-836B-7	Sequence 7, Appli
43	62	12.0	428	4	US-09-370-265-7	Sequence 7, Appli
44	62	12.0	428	4	US-09-357-800C-7	Sequence 7, Appli
45	62	12.0	428	4	US-09-370-625A-7	Sequence 7, Appli

ALIGNMENTS

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RESULT 1
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; Sequence 21, Application US/09166350A
; Patent No. 6440663
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Chen, Yao
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Old, Lloyd
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alex
; TITLE OF INVENTION: Renal Cancer Associated Antigens and
; FILE REFERENCE: 10461/7051
; CURRENT APPLICATION NUMBER: US/09/166,350A
; EARLIER FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: US 09/166,350
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-350-21
Query Match      100.0%; Score 517; DB 4; Length 206;
Best Local Similarity 100.0%; Pred. No. 8.7e-64;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      9 TYVCLANVLGRKLSDFIDPQGWKLAVALKPSGDRYNOFHIRREALLQTKSPPTS 68
        61 ELLPDMGTTNCTVGDVLDLIIQNEFPAPASLLPDVAVP 98
DB      69 ELFPDMGTTNCTVGDVLDLIIQNEFPAPASLLPDVAVP 106
RESULT 2
US-09-135-232-2
; Sequence 2, Application US/09135232
; Patent No. 6262228
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaodan
; TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods
; FILE REFERENCE: 798-019
; CURRENT APPLICATION NUMBER: US/09/135,232
; CURRENT FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 2
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 596
TYPE: PRT
ORGANISM: human
US-09-135-232-2

Query Match 18.7%; Score 96.5; DB 3; Length 596;
Best Local Similarity 31.5%; Pred. No. 0.00019;
Matches 23; Conservative 12; Mismatches 31; Indels 7; Gaps 1;

QY 8 VGLIRKSDPFDPEBGMKLAVALKKSQDDRYNOFHRRFALLQTKSPTELLPDWG 67
DB 25 LGEICAVLDSCDGLGWRGLAERLSS-----SWLDVRIHEKYVDQKSGSTRILLMSWA 77

QY 68 TTNCTVGDVLVDLL 80
DB 78 QKNKTIIDLLQVYL 90

RESULT 3

US-09-863-549-2
Sequence 2, Application US/09863549
Patent No. 6576444
GENERAL INFORMATION:
APPLICANT: Cao, Zhaoan
TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods
FILE REFERENCE: T98-019
CURRENT APPLICATION NUMBER: US/09/863,549
CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: 09/135,232
PRIOR FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 596
TYPE: PRT
ORGANISM: human
US-09-863-549-2

Query Match 18.7%; Score 96.5; DB 4; Length 596;
Best Local Similarity 31.5%; Pred. No. 0.00019;
Matches 23; Conservative 12; Mismatches 31; Indels 7; Gaps 1;

QY 8 VGLIRKSDPFDPEBGMKLAVALKKSQDDRYNOFHRRFALLQTKSPTELLPDWG 67
DB 25 LGEICAVLDSCDGLGWRGLAERLSS-----SWLDVRIHEKYVDQKSGSTRILLMSWA 77

QY 68 TTNCTVGDVLVDLL 80
DB 78 QKNKTIIDLLQVYL 90

RESULT 4

US-08-980-060-2
Sequence 2, Application US/08980060
Patent No. 5965421
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: FENG, PING
APPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,060
FILING DATE: Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 590 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-980-060-2

Query Match 15.3%; Score 79; DB 2; Length 590;
Best Local Similarity 31.9%; Pred. No. 0.051;
Matches 22; Conservative 12; Mismatches 19; Indels 16; Gaps 2;

QY 45 IRREFALLQTKSPTELLPDWGTTNCTVGDVLVDLLQNEFPAPASLL----- 93

DB 42 LKIKSMERVOQSVSTIRELLMMWGMKRAVQQLVDLLCRLELYRAAQIILNWKPAEIRIC 101

QY 94 -----PDAY 97
DB 102 PIPAPPDVY 110

RESULT 5

US-09-307-185-2
Sequence 2, Application US/09307185
Patent No. 6222019
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: FENG, PING
APPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/307,185
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/980,060
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:

RESULT 9
US-09-773-4
Sequence 4, Application US/09773753
Patent No. 6653452
GENERAL INFORMATION:
APPLICANT: NI, JIAN
FENG, PING
MUZIO, MARTA
DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/773,753
FILING DATE: 02-Feb-2001
CLASSIFICATION: <Unknown>

[illegible]

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Best Local Similarity 31.1%; Pred. NO. 0.62;
Matches 41; Conservative 13; Mismatches 37; Indels 41; Gaps 10;

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Db 167 VRRWDVSLVEGLPDPDMKIAFERFWLKTSNELIAENV-KAQGDMAAIRKNANE-RILEAY 224
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 52 LQ-----TGKSPISLELLFDWGTN---CTVGDIVDLLIONE-----FFAP----- 88
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 225 LDQAEWIATGVHPTDEVDYINNGTIPNTGMCVL-NILPELLGSHPLPIDILEQLFLPSRFRH 283
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 89 ----ASLLLPDA 96
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 284 LIELASRLVDAA 295
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```


APPLICANT: Croteau, Rodney B
 APPLICANT: Crock, John E
 APPLICANT: Bohlman, Jorg
 APPLICANT: Jetter, Reinhard
 APPLICANT: Steele, Christopher L
 TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
 TITLE OF INVENTION: AND METHODS OF USE
 FILE REFERENCE: MSUR11345
 CURRENT APPLICATION NUMBER: US/09/234,393A
 CURRENT FILING DATE: 1999-01-20
 EARLIER APPLICATION NUMBER: 60/072,204
 EARLIER FILING DATE: 1998-01-22
 NUMBER OF SEQ ID NOS: 55
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 54
 LENGTH: 593
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:
 OTHER INFORMATION: protein
 FEATURE:
 NAME/KEY: misc. feature
 LOCATION: (1)..(817)
 OTHER INFORMATION: Computer-generated protein sequence
 US-09-234-393-54

Query Match 13.4%; Score 69.5; DB 3; Length 593;
 Best Local Similarity 31.1%; Pred. No. 1.1;
 Matches 41; Conservative 13; Mismatches 37; Indels 41; Gaps 10;

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 DB 362 VRRMVSIVLEGLPDFMKIAFEFLKTSNELIABAV-KAOGQDMAVYIRKNAME-RYLEAY 419
 QY 52 IQ-----TKSPTSELLFDWGTN---CTVGDVLDLLIONE-----FFAP----- 88
 DB 420 LQDAEWIATGHWPTDEYLNNGTPNTGMCVL-NLIPLLMGHEHLPIDILEQIFLPSRFHH 478
 QY 89 ----ASLLLPDA 96
 DB 479 LIELASRLVDDA 490

RESULT 15
 US-09-865-171-24
 ; Sequence 24, Application US/09865171
 ; Patent No. 6451576
 ; GENERAL INFORMATION:
 ; APPLICANT: Croteau, Rodney B
 ; APPLICANT: Crock, John E
 ; APPLICANT: Bohlman, Jorg
 ; APPLICANT: Steele, Christopher L
 ; TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS),
 ; TITLE OF INVENTION: AND METHODS OF USE
 ; FILE REFERENCE: MSUR117468
 ; CURRENT APPLICATION NUMBER: US/09/865,171
 ; CURRENT FILING DATE: 2001-05-24
 ; PRIOR APPLICATION NUMBER: 09/234,393
 ; PRIOR FILING DATE: 1999-01-20
 ; PRIOR APPLICATION NUMBER: 60/072,204
 ; PRIOR FILING DATE: 1998-01-22
 ; NUMBER OF SEQ ID NOS: 55
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 24
 ; LENGTH: 593
 ; TYPE: PRT
 ; ORGANISM: Abies grandis
 ; US-09-865-171-24

Query Match 13.4%; Score 69.5; DB 4; Length 593;
 Best Local Similarity 31.1%; Pred. No. 1.1;
 Matches 41; Conservative 13; Mismatches 37; Indels 41; Gaps 10;

QY 3 VRCLNVGLIRKLSDFID-POEGWKK-----LAVAIIKPSGSD-----RYNQFHRRPEAL 51
 DB 362 VRRMVSIVLEGLPDFMKIAFEFLKTSNELIABAV-KAOGQDMAVYIRKNAME-RYLEAY 419
 QY 52 IQ-----TKSPTSELLFDWGTN---CTVGDVLDLLIONE-----FFAP----- 88
 DB 420 LQDAEWIATGHWPTDEYLNNGTPNTGMCVL-NLIPLLMGHEHLPIDILEQIFLPSRFHH 478
 QY 89 ----ASLLLPDA 96
 DB 479 LIELASRLVDDA 490

Search completed: January 10, 2005, 23:26:36
 Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 10, 2005, 23:25:15 ; Search time 145 Seconds
(without alignments)
243.696 Million cell updates/sec

Title: US-10-001-254-6
Perfect score: 517
Sequence: 1 TYVRCINLVGLIRKLSDFIDP.....LLIIONEFAPASLLLPDAPV 98

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	517	100.0	460	14	US-10-001-254-16
3	517	100.0	460	14	US-10-001-254-28
4	513	99.2	460	9	US-09-795-595-1
5	513	99.2	460	10	US-09-759-595-1
6	476	92.1	459	9	US-09-795-595-3
7	476	92.1	459	10	US-09-759-595-3
8	247	47.8	59	14	US-10-001-254-26
9	96.5	18.7	596	9	US-09-863-549-2
10	96.5	18.7	644	15	US-10-425-114-54258
11	95	18.4	609	14	US-10-340-545-2
12	79	15.3	590	9	US-09-773-753-2
13	79	15.3	590	14	US-10-366-288-20

14	79	15.3	590	16	US-10-657-146-2	Sequence 2, Appl1
15	79	15.3	625	9	US-09-773-753-4	Sequence 4, Appl1
16	79	15.3	625	16	US-10-657-146-4	Sequence 4, Appl1
17	72.5	14.0	824	14	US-10-024-298A-131	Sequence 131, App
18	72.5	14.0	824	14	US-10-042-211A-131	Sequence 131, App
19	72.5	14.0	824	15	US-10-617-217A-131	Sequence 131, App
20	72.5	14.0	824	17	US-10-024-298A-131	Sequence 131, App
21	72.5	14.0	928	16	US-10-437-963-152971	Sequence 152971, App
22	71.5	13.8	5836	15	US-10-378-083-20	Sequence 23, Appl1
23	71	13.7	259	9	US-09-987-107-23	Sequence 23, Appl1
24	71	13.7	259	14	US-10-316-253-277	Sequence 277, App
25	71	13.7	259	14	US-10-316-253-285	Sequence 285, App
26	71	13.7	259	14	US-10-316-253-287	Sequence 287, App
27	71	13.7	259	14	US-10-316-253-289	Sequence 289, App
28	69.5	13.4	398	14	US-10-025-145A-20	Sequence 20, Appl1
29	69.5	13.4	593	9	US-09-865-171-24	Sequence 24, Appl1
30	69.5	13.4	593	9	US-09-865-171-50	Sequence 50, Appl1
31	69.5	13.4	593	9	US-09-865-171-52	Sequence 52, Appl1
32	69.5	13.4	593	9	US-09-865-171-54	Sequence 54, Appl1
33	69.5	13.4	593	9	US-09-895-752-50	Sequence 50, Appl1
34	69.5	13.4	593	9	US-09-887-586A-50	Sequence 50, Appl1
35	69.5	13.4	593	9	US-09-903-012-50	Sequence 50, Appl1
36	69.5	13.4	593	10	US-09-900-797-50	Sequence 50, Appl1
37	69.5	13.4	593	11	US-09-893-820-50	Sequence 50, Appl1
38	69.5	13.4	593	13	US-10-041-007-20	Sequence 20, Appl1
39	68.5	13.2	964	16	US-10-437-963-119980	Sequence 119980, App
40	67.5	13.1	413	16	US-10-437-963-186825	Sequence 186825, App
41	67.5	13.1	527	9	US-09-815-242-11374	Sequence 11374, A
42	67.5	13.1	527	15	US-10-282-122A-58815	Sequence 58815, A
43	67.5	13.1	733	16	US-10-437-963-142702	Sequence 142702, App
44	67.5	13.1	813	16	US-10-437-963-142703	Sequence 142703, App
45	67.5	13.1	813	16	US-10-437-963-186828	Sequence 186828, App

ALIGNMENTS

RESULT 1
US-10-001-254-6
Sequence 6, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sug Hyung
; APPLICANT: Roch, Wilfried
; APPLICANT: Steiner-Liwen, Frank
; TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-1J 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-254-6

Query Match 100.0%; Score 517; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.5e-57;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TYVRCINLVGLIRKLSDFIDPQEGWKLVAIAIKKSGDRYQFIRRFALLQTKSPTS 60
1 TYVRCINLVGLIRKLSDFIDPQEGWKLVAIAIKKSGDRYQFIRRFALLQTKSPTS 60

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QY 61 ELFPDMGTTNCTVGDVLDLIIQNEFFAPASILLPDVAVP 98
DB 61 ELFPDMGTTNCTVGDVLDLIIQNEFFAPASILLPDVAVP 98

RESULT 2
US-10-001-254-16
; Sequence 16, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sung Hyung
; APPLICANT: Roth, Wilfred
; APPLICANT: Stenmer-Llewellyn, Frank
; TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-254-16

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Best Local Similarity 100.0%; Pred. No. 3.3e-56;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 9 TYVRCINVLGIRKLSDFIDPQSGWKLAIAIKKPSGDDRYNQFHRRFEALLQTKSPTS 68

QY 61 ELFPDMGTTNCTVGDVLDLIIQNEFFAPASILLPDVAVP 98
DB 61 ELFPDMGTTNCTVGDVLDLIIQNEFFAPASILLPDVAVP 106

RESULT 3
US-10-001-254-28
; Sequence 28, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sung Hyung
; APPLICANT: Roth, Wilfred
; APPLICANT: Stenmer-Llewellyn, Frank
; TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-254-28
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Query Match 100.0%; Score 517; DB 14; Length 460;
Best Local Similarity 100.0%; Pred. No. 3.3e-56;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 9 TYVRCINVLGIRKLSDFIDPQSGWKLAIAIKKPSGDDRYNQFHRRFEALLQTKSPTS 68

QY 61 ELFPDMGTTNCTVGDVLDLIIQNEFFAPASILLPDVAVP 98
DB 61 ELFPDMGTTNCTVGDVLDLIIQNEFFAPASILLPDVAVP 106

RESULT 4
US-09-795-595-1
; Sequence 1, Application US/09795595
; Publication No. US20020039423A1
; GENERAL INFORMATION:
; APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT APPLICATION NUMBER: US/09/795,595
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/176,395
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-595-1

Query Match 99.2%; Score 513; DB 9; Length 460;
Best Local Similarity 99.0%; Pred. No. 1.1e-55;
Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TYVRCINVLGIRKLSDFIDPQSGWKLAIAIKKPSGDDRYNQFHRRFEALLQTKSPTS 60
DB 9 TYVRCINVLGIRKLSDFIDPQSGWKLAIAIKKPSGDDRYNQFHRRFEALLQTKSPTS 68

QY 61 ELFPDMGTTNCTVGDVLDLIIQNEFFAPASILLPDVAVP 98
DB 61 ELFPDMGTTNCTVGDVLDLIIQNEFFAPASILLPDVAVP 106

RESULT 5
US-09-759-595-1
; Sequence 1, Application US/09759595
; Publication No. US20030059916A1
; GENERAL INFORMATION:
; APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT APPLICATION NUMBER: US/09/759,595
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/176,395
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-595-1

Query Match 99.2%; Score 513; DB 10; Length 460;
Best Local Similarity 99.0%; Pred. No. 1.1e-55;
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Matches	97: Conservative	0: Mismatches	1: Indels	0: Gaps	0:
Qy	1	TYVCLVNGLRKLSDFIDPOEGWKLAVALIKPSGDRVYNOQFHRREALLQTKSPTS	60		
Db	9	TYVCLVNGLRKLSDFIDPOEGWKLAVALIKPSGDRVYNOQFHRREALLQTKSPTS	68		
Qy	61	ELFPDMGTTNCVGLVDLLIQNEFFAPASLLLPAPV	98		
Db	69	ELFPDMGTTNCVGLVDLLIQNEFFAPASLLLPAPV	106		

RESULT 6
US-09-795-595-3
Sequence 3, Application US/09795595
Publication No. US20020039423A1
GENERAL INFORMATION:
APPLICANT: Wesche, Holger
APPLICANT: Li, Shyun
APPLICANT: Tulajar Inc.
TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
FILE REFERENCE: 018781-003910US
CURRENT APPLICATION NUMBER: US/09/795,595
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 459
TYPE: PRT
ORGANISM: Mus sp.
US-09-795-595-3

	Query Match	92.1%;	Score 476;	DB 9;	Length 459;	
	Best Local Similarity	90.8%;	Pred. No. 4,9e-51;			
	Matches	Conservative	5;	Mismatches	4;	Indels 0; Gaps 0;
Qy	1	TYVCCINLVGIRKISDFIDPOEGMKCLVAIKKPSGDGRYNQFHRRFEALLQTCKSTPS	60			
Dd	9	TYIRNLNVGIARKSDFIIDPOEGMKCLVAIKKPSGDGRYNQFHIRREBALLQTCKSTFC	68			
Qy	61	ELLFDWGTTCNCTGVLDVLILIONEFPAPASLLPDPVP	98			
Dd	69	ELLFDWGTTCNCTGVLDVLIVQIELFAPATLLLPDPVP	106			

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RESULT 7
US-09-759-595-3
: Sequence 3, Application US/09759595
: Publication No. US20030059916A1
: GENERAL INFORMATION:
: APPLICANT: Wesche, Holger
: APPLICANT: Li, Shyun
: TITLE OF INVENTION: RAK-4: Compositions and Methods of Use
: FILE REFERENCE: 018781-003910US
: CURRENT APPLICATION NUMBER: US/09/759,595
: CURRENT FILING DATE: 2001-01-13
: PRIOR APPLICATION NUMBER: US 60/176,395
: PRIOR FILING DATE: 2000-01-13
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3
: LENGTH: 459
: TYPE: PRT
: ORGANISM: Mus sp.
US-09-759-595-3

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Query Match	92.1%	Score 476	DB 10	Length 459
Beat Local Similarity	90.8%	Pred. No. 4,9e-51		
Matches	89	Conservative	4	Indels 0
		Mismatches	4	Gaps 0

[illegible]

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RESULT 8
US-10-001-254-26
; Sequence 26, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sung Hyung
; APPLICANT: Roth, Wilfried
; APPLICANT: Stemmer-Lieween, Frank
; TITLE OF INVENTION: No. US20030049702A1el Death Domain Proteins
; FILE REFERENCE: P-IJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; PRIOR APPLICATION NUMBER: 2001-11-15
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-254-26

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Query Match          47.8%; Score 247; DB 14; Length 59;
Best Local Similarity 100.0%; Pred. No. 2,9e-23;
Matches    46; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

Oy      1  TYVACLNVGLIRKLSDFIDPQSGWKKLAVALIKKPSGDDRYNQPHIR 46
        |||||
Db       9  TYVACLVNGLIRKLSDFIDPQSGWKKLAVAIKKSPGDDRYNQPHIR 54
        |||||

RESULT 9
US-09-863-549-2
Sequence 2, Application US/09863549
Patent No. US20020049330A1
GENERAL INFORMATION:
APPLICANT: Cao, Zhaoan
TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods
FILE REFERENCE: T98-019
CURRENT APPLICATION NUMBER: US/09/863,549
CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: 09/135,232
PRIOR FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 596
TYPE: PRT
ORGANISM: human
US-09-863-549-2
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Query Match	18.7%	Score 96.5	DB 9.5	Length 596
Best Local Similarity	31.5%	Pred. No. 0.0056		
Matches	23	Conservative	12	Mismatches 31; Indels 7; Gaps 1;
Cy	8	VGILRKLSDFDPBEGMKKLAVALIKESGDDRYNQFHRRREALLQTKSPSTSLLDWG	67	
Db	25	IGELCAVLDSCDGALGWRGLAERLTS-----SWLDVRHIEKVDQSGSTRELSMA	77	

? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/980,060
 ? FILING DATE: Herewith
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: STEERE, ERIC K.
 ? REGISTRATION NUMBER: 36,688
 ? REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
 ?

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;          TOPOLOGY: Linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-773-753-4

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Query Match	15.3%;	Score 79;	DB 9;	Length 625;
Best Local Similarity	31.9%;	Pred. No.	0.96;	

Matches	22;	Conservative	12;	Mismatches	19;	Indels	16;	Gaps	2;
Qy	45	IRRFALLQT-GKSPTELLPDMGTNCTVGDVLDLLIQNEFFAPASLL-----	93						
Db	42	LRKIKSMERVQGVSIITRELLMWMGMQATVQQLVDLLCRLELYRAAQIILNMKPAPEIRC	101						
Qy	94	-----PDAV 97							
Db	102	PIPAFPDSV 110							

Search completed: January 10, 2005, 23:37:31
 Job time : 146 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: January 12, 2005, 08:09:24 ; Search time 465 Seconds

(without alignments)
1210.961 Million cell updates/sec

Title: US-10-001-254-6

Perfect score: 1 TYVRCINVGIRKUSDFIDP.....LLINERFAPASILLPDAVP 98

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10001254@cgn_1_1.480@runat_10012005.172741.10536
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7

Database :

Published Applications NA.*
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12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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16: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
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19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517	100.0	294	14 US-10-001-254-5	Sequence 5, Appl1
2	517	100.0	1383	14 US-10-001-254-15	Sequence 15, Appl1
3	517	100.0	2817	10 US-09-966-451-3	Sequence 3, Appl1
4	517	100.0	2817	14 US-10-001-254-27	Sequence 27, Appl1
5	517	100.0	2817	16 US-10-630-399-3	Sequence 2, Appl1
6	513	99.2	1383	9 US-09-795-595-2	Sequence 2, Appl1
7	513	99.2	1383	10 US-09-759-595-2	Sequence 2, Appl1
8	476	92.1	1542	9 US-09-759-595-4	Sequence 4, Appl1
9	476	92.1	1542	10 US-09-759-595-4	Sequence 4, Appl1
10	413	79.9	501	9 US-09-833-790-149	Sequence 149, Appl1
11	256	49.5	31000	16 US-10-966-451-10	Sequence 10, Appl1
12	256	49.5	31000	16 US-10-630-399-10	Sequence 10, Appl1
13	247	47.8	211	14 US-10-001-254-25	Sequence 25, Appl1
14	247	47.8	470	16 US-10-242-535A-26096	Sequence 26096, A
15	247	47.8	470	16 US-10-085-783A-26096	Sequence 26096, A
16	134.5	26.0	408	11 US-09-969-034-428	Sequence 428, Appl1
17	96.5	18.7	2288	9 US-09-863-549-1	Sequence 1, Appl1
18	96.5	18.7	2292	13 US-10-098-841-3	Sequence 3, Appl1
19	96.5	18.7	2406	16 US-10-425-114-26259	Sequence 26259, A
20	95	18.4	1888	15 US-10-340-545-1	Sequence 1, Appl1
21	79.5	15.4	476	14 US-10-198-846-1432	Sequence 1432, Appl1
22	79	15.3	1782	15 US-10-366-288-19	Sequence 19, Appl1
23	79	15.3	1806	9 US-09-773-753-1	Sequence 1, Appl1
24	79	15.3	1806	17 US-10-657-146-1	Sequence 1, Appl1
25	79	15.3	3459	9 US-09-773-753-3	Sequence 3, Appl1
26	79	15.3	3459	17 US-10-657-146-3	Sequence 3, Appl1
27	78.5	15.2	479	17 US-10-657-146-14	Sequence 14, Appl1
28	78.5	15.2	479	17 US-10-657-146-14	Sequence 14, Appl1
29	78.5	15.2	708	16 US-10-424-599-384	Sequence 384, Appl1
30	78.5	15.2	861	9 US-09-764-877-3589	Sequence 3589, Appl1
31	78.5	15.2	861	16 US-10-242-515-3589	Sequence 3589, Appl1
32	78.5	15.2	864	9 US-09-764-877-3587	Sequence 3587, Appl1
33	78.5	15.2	864	9 US-09-764-877-3590	Sequence 3590, Appl1
34	78.5	15.2	864	16 US-10-242-515-3587	Sequence 3587, Appl1
35	78.5	15.2	864	16 US-10-242-515-3587	Sequence 3590, Appl1
36	74.5	14.6	3128	16 US-10-108-260A-709	Sequence 709, Appl1
37	74.5	14.4	774	9 US-09-974-300-1011	Sequence 1011, Appl1
38	73.5	14.2	1153	17 US-10-437-963-83917	Sequence 83917, A
39	73	14.1	497	13 US-10-027-632-50723	Sequence 50723, A
40	73	14.1	497	13 US-10-027-632-50723	Sequence 50723, A
41	73	14.1	497	13 US-10-027-632-50723	Sequence 50723, A
42	73	14.1	497	15 US-10-027-632-50724	Sequence 50724, A
43	73	14.1	499	13 US-10-027-632-72567	Sequence 72567, A
44	73	14.1	499	13 US-10-027-632-72568	Sequence 72568, A
45	73	14.1	499	15 US-10-027-632-72567	Sequence 72567, A

ALIGNMENTS

RESULT 1
US-10-001-254-5
; Sequence 5, Application US/10001254
; Publication No. US20030049702A1
GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sung Hyung
; APPLICANT: Roth, Wilfried
; APPLICANT: Stehner-Liwen, Frank
; TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US/10/001,254
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 62

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 294
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (294)
US-10-001-254-5

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Alignment Scores:

Pred. No.:	2,69e-71	Length:	294
Score:	517.00	Matches:	98
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-10-001-254-6 (1-98) x US-10-001-254-5 (1-294)

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QY 1 ThTyrValArgCysLeuAenValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20
DB 1 ACATATGTGGCGCTGCTCAATGTTGACTAATTGAGAGCTGTGACATTTTATTGATCCT 60
QY 21 GlnGlnGlyTTPlySylsLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
DB 61 CAAGAAGAGTGAAGAAGATTGAGTGTGATTAATAAACCACTGTGATGATGATGATAC 120
QY 41 AenGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnThrGlyLysSerProThrSer 60
DB 121 AATCATGTTTCACATTAAGAGATTGAGCACTTACTTAACCTGAAAAAGTCCCACTTCT 180
QY 61 GluLeuLeuPheAspTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80
DB 181 GAATTACTGTTTGACTGGGGCACCAAAATTGCAGTTGCTGATCTTGTGATCTTTTG 240
QY 81 IleglnAsnGluPhePheAlaProAlaSerLeuLeuProAspAlaValPro 98
DB 241 ATCCAAATGAAATTTTTCCTCTCGAGCTTTTGTCTCCAGATGCTGTTCCC 294

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RESULT 2

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US-10-001-254-15
; Sequence 15, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sung Hyung
; APPLICANT: Roth, Wilfred
; APPLICANT: Stemmer-Ulrich, Frank
; TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-Ld 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1383
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (1380)
US-10-001-254-15

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Alignment Scores:

Pred. No.:	2,48e-70	Length:	1383
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Score:	517.00	Matches:	98
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-10-001-254-6 (1-98) x US-10-001-254-15 (1-1383)

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QY 1 ThTyrValArgCysLeuAenValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20
DB 25 ACATATGTGGCGCTGCTCAATGTTGACTAATTGAGAGCTGTGACATTTTATTGATCCT 84
QY 21 GlnGlnGlyTTPlySylsLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
DB 85 CAAGAAGAGTGAAGAAGATTGAGTGTGATTAATAAACCACTGTGATGATGATGATAC 144
QY 41 AenGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnThrGlyLysSerProThrSer 60
DB 145 AATCATGTTTCACATTAAGAGATTGAGCACTTACTTAACCTGAAAAAGTCCCACTTCT 204
QY 61 GluLeuLeuPheAspTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80
DB 205 GAATTACTGTTTGACTGGGGCACCAAAATTGCAGTTGCTGATCTTGTGATCTTTTG 264
QY 81 IleglnAsnGluPhePheAlaProAlaSerLeuLeuProAspAlaValPro 98
DB 265 ATCCAAATGAAATTTTTCCTCTCGAGCTTTTGTCTCCAGATGCTGTTCCC 318

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RESULT 3

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US-09-966-451-3
; Sequence 3, Application US/09966451
; Publication No. US20030087856A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freter
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 (EXPRESS)
; FILE REFERENCE: RTS-0324
; CURRENT APPLICATION NUMBER: US/09/966,451
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50) ... (1432)
US-09-966-451-3

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Alignment Scores:

Pred. No.:	6,87e-70	Length:	2817
Score:	517.00	Matches:	98
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-001-254-6 (1-98) x US-09-966-451-3 (1-2817)

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QY 1 ThTyrValArgCysLeuAenValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20
DB 74 ACATATGTGGCGCTGCTCAATGTTGACTAATTGAGAGCTGTGACATTTTATTGATCCT 133
QY 21 GlnGlnGlyTTPlySylsLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
DB 134 CAAGAAGAGTGAAGAAGATTGAGTGTGATTAATAAACCACTGTGATGATGATGATAC 193
QY 41 AenGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnThrGlyLysSerProThrSer 60
DB 194 AATCATGTTTCACATTAAGAGATTGAGCACTTACTTAACCTGAAAAAGTCCCACTTCT 253
QY 61 GluLeuLeuPheAspTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80

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Db      254 GAATTACTGTTTGACGGGGGACCAAAATTCAGACAGTTGGTGAATCTTGATCTTTTG 313
Qy      81 11leGlnAngluPhePheAlaProAlaSerLeuLeuLeuProAlaValPro 98
Db      314 ATCCAAATGAATTTTGTCTCGCGAGTCTTTTGCTCCAGATGCTGTTCCC 367

RESULT 4
US-10-001-254-27
; Sequence 27, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawloweki, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sug Hyung
; APPLICANT: Roch, Wilfred
; APPLICANT: Stenner-Liewen, Frank
; TITLE OF INVENTION: No. US20030049702A1el Death Domain Proteins
; FILE REFERENCE: P-1J 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50) ... (1429)
; US-10-001-254-27

Alignment Scores:
Pred. No.: 6.87e-70 Length: 2817
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 14

US-10-001-254-6 (1-98) x US-10-001-254-27 (1-2817)

Qy      1 ThrtYrValArgCySLeuAenValGlyLeuIlleArgLysLeuSerAspPheIlleAspPro 20
Db      74 ACATATGCGCGCTGCTCAATGTTGACTAATTAGGAAGCTGTGCAGATTTTATTGATCTT 133
Qy      21 GlnGlnGlyTTPlyLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
Db      134 CAAGAAGATGGAAGAATTGAGTGTACTTATTAATAAACCATCTGGTGATGATGATGATAC 193
Qy      41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnIntrGlyLysSerProThrSer 60
Db      194 AATAGATTTCATTAAGAGATTGAAACATTACTTCAACTGGAAGAAAGTCCCACTTCT 253
Qy      61 GluLeuLeuPheAspTTPGlyThrThrAsnCySThrValGlyAspLeuValAspLeuLeu 80
Db      254 GAATTACTGTTTGACGGGGACCAAAATTCAGACAGTTGGTGAATCTTGATCTTTTG 313
Qy      81 11leGlnAngluPhePheAlaProAlaSerLeuLeuLeuProAlaValPro 98
Db      314 ATCCAAATGAATTTTGTCTCGCGAGTCTTTTGCTCCAGATGCTGTTCCC 367

RESULT 5
US-10-630-399-3
; Sequence 3, Application US/10630399
; Publication No. US20040019009A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett

```

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; APPLICANT: Susan M. Freter
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
; FILE REFERENCE: RRS-0324
; CURRENT APPLICATION NUMBER: US/10/630,399
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/966,451
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50) ... (1432)
; US-10-630-399-3

Alignment Scores:
Pred. No.: 6.87e-70 Length: 2817
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 16

US-10-001-254-6 (1-98) x US-10-630-399-3 (1-2817)

Qy      1 ThrtYrValArgCySLeuAenValGlyLeuIlleArgLysLeuSerAspPheIlleAspPro 20
Db      74 ACATATGCGCGCTGCTCAATGTTGACTAATTAGGAAGCTGTGCAGATTTTATTGATCTT 133
Qy      21 GlnGlnGlyTTPlyLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
Db      134 CAAGAAGATGGAAGAATTGAGTGTACTTATTAATAAACCATCTGGTGATGATGATGATAC 193
Qy      41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnIntrGlyLysSerProThrSer 60
Db      194 AATAGATTTCATTAAGAGATTGAAACATTACTTCAACTGGAAGAAAGTCCCACTTCT 253
Qy      61 GluLeuLeuPheAspTTPGlyThrThrAsnCySThrValGlyAspLeuValAspLeuLeu 80
Db      254 GAATTACTGTTTGACGGGGACCAAAATTCAGACAGTTGGTGAATCTTGATCTTTTG 313
Qy      81 11leGlnAngluPhePheAlaProAlaSerLeuLeuLeuProAlaValPro 98
Db      314 ATCCAAATGAATTTTGTCTCGCGAGTCTTTTGCTCCAGATGCTGTTCCC 367

RESULT 6
US-09-795-595-2
; Sequence 2, Application US/09795595
; Publication No. US20020039423A1
; GENERAL INFORMATION:
; APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT APPLICATION NUMBER: US/09/795,595
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/176,395
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1383
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human IL-1 receptor-associated kinase 4 (IRAK-4)
; NAME/KEY: CDS
; LOCATION: (1) ... (1383)
; OTHER INFORMATION: human IRAK-4

```

US-09-795-595-2

Alignment Scores:
Pred. No.: 1,05e-69 Length: 1383
Score: 513.00 Matches: 97
Percent Similarity: 98.98% Conservative: 0
Best Local Similarity: 98.98% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 9 Gaps: 0

US-10-001-254-6 (1-98) x US-09-795-595-2 (1-1383)

QY 1 ThrTYValArgCYLeuAsnValGlyLeuIleArgLYsLeuSerAspPheIleAspPro 20
DB 25 ACATATGTCGCGCTCCTCAATGTTGAGCTAATTAGAAAGCTGTGCAGATTTATTGATCCT 84
QY 21 GlnGlnGlyTTPlyLysLeuAlaValAlaIleLysLYsProSerGlyAspAspArgTYr 40
DB 85 CAAGAAGATGGAGAGATTAGCTGATTAATAAACATCTGGTGTGATGATGATAC 144
QY 41 AengInPheHsiIleArgArgPheGlnAlaLeuLeuGlnThrGlyLYsSerProThrSer 60
DB 145 AATCAGTTTCACATAAGAGATTGAGACTTCTCAACCTGAAAAAGTCCCACTTCT 204
QY 61 GluLeuLeuPheAspTTPGlyThrThrAsnCYsThrValGlyAspLeuValAspLeu 80
DB 205 GAATTACTGTTGACTGGGCGACCAAAATTCACAGCTGTGATCTTGTGATCTTTTG 264
QY 81 IlegInaEngLuphePheAlaProAlaSerLeuLeuProAspAlaValPro 98
DB 265 ATCCAAATGAATTTTGTCTCTCGAGCTTTTGTCTCCCAAGATGCTGTTC 318

RESULT 7

US-09-759-595-2
; Sequence 2, Application US/09759595
; Publication No. US20030059916A1
; GENERAL INFORMATION:
; APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 60/176,395
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1383
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human IL-1 receptor-associated kinase 4 (IRAK-4)
; NAME/KEY: CDS
; LOCATION: (1)..(1383)
; OTHER INFORMATION: human IRAK-4
US-09-759-595-2

Alignment Scores:
Pred. No.: 1,05e-69 Length: 1383
Score: 513.00 Matches: 97
Percent Similarity: 98.98% Conservative: 0
Best Local Similarity: 98.98% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 10 Gaps: 0

US-10-001-254-6 (1-98) x US-09-759-595-2 (1-1383)

QY 1 ThrTYValArgCYLeuAsnValGlyLeuIleArgLYsLeuSerAspPheIleAspPro 20
DB 25 ACATATGTCGCGCTCCTCAATGTTGAGCTAATTAGAAAGCTGTGCAGATTTATTGATCCT 84

DB 25 ACATATGTCGCGCTCCTCAATGTTGAGCTAATTAGAAAGCTGTGCAGATTTATTGATCCT 84

QY 21 GlnGlnGlyTTPlyLysLeuAlaValAlaIleLysLYsProSerGlyAspAspArgTYr 40
DB 85 CAAGAAGATGGAGAGATTAGCTGATTAATAAACATCTGGTGTGATGATGATAC 144
QY 41 AengInPheHsiIleArgArgPheGlnAlaLeuLeuGlnThrGlyLYsSerProThrSer 60
DB 145 AATCAGTTTCACATAAGAGATTGAGACTTCTCAACCTGAAAAAGTCCCACTTCT 204

QY 61 GluLeuLeuPheAspTTPGlyThrThrAsnCYsThrValGlyAspLeuValAspLeu 80

DB 205 GAATTACTGTTGACTGGGCGACCAAAATTCACAGCTGTGATCTTGTGATCTTTTG 264

QY 81 IlegInaEngLuphePheAlaProAlaSerLeuLeuProAspAlaValPro 98

DB 265 ATCCAAATGAATTTTGTCTCTCGAGCTTTTGTCTCCCAAGATGCTGTTC 318

RESULT 8

US-09-795-595-4
; Sequence 4, Application US/09795595
; Publication No. US20020039423A1
; GENERAL INFORMATION:
; APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/176,395
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4)
; NAME/KEY: CDS
; LOCATION: (163)..(1542)
; OTHER INFORMATION: murine IRAK-4
US-09-795-595-4

Alignment Scores:
Pred. No.: 7,87e-64 Length: 1542
Score: 476.00 Matches: 89
Percent Similarity: 95.92% Conservative: 5
Best Local Similarity: 90.82% Mismatches: 4
Query Match: 92.07% Indels: 0
DB: 9 Gaps: 0

US-10-001-254-6 (1-98) x US-09-795-595-4 (1-1542)

QY 1 ThrTYValArgCYLeuAsnValGlyLeuIleArgLYsLeuSerAspPheIleAspPro 20
DB 187 ACATATGTCGCGCTCCTCAATGTTGAGCTAATTAGAAAGCTGTGCAGATTTATTGATCCT 246
QY 21 GlnGlnGlyTTPlyLysLeuAlaValAlaIleLysLYsProSerGlyAspAspArgTYr 40
DB 247 CAAGAAGATGGAGAGATTAGCTGATTAATAAACATCTGGTGTGATGATGATAC 306
QY 41 AengInPheHsiIleArgArgPheGlnAlaLeuLeuGlnThrGlyLYsSerProThrSer 60
DB 307 AATCAGTTTCACATAAGAGATTGAGACTTCTCAACCTGAAAAAGTCCCACTTCT 366
QY 61 GluLeuLeuPheAspTTPGlyThrThrAsnCYsThrValGlyAspLeuValAspLeu 80
DB 367 GAATTACTGTTGACTGGGCGACCAAAATTCACAGCTGTGATCTTGTGATCTTTTG 426
QY 81 IlegInaEngLuphePheAlaProAlaSerLeuLeuProAspAlaValPro 98

Db 427 GTCCAGATTGAGCTGTTGGCCCGGACACTCTCGGCTGGCGGATGCGTTCCC 480

RESULT 9
US-09-759-595-4
; Sequence 4, Application US/09759595
; Publication No. US20030059916A1
; GENERAL INFORMATION:
; APPLICANT: Weeche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT APPLICATION NUMBER: US/09/759,595
; PRIOR FILING DATE: 2001-01-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4)
; NAME/KEY: CDS
; LOCATION: (163)..(1542)
; OTHER INFORMATION: murine IRAK-4
US-09-759-595-4

Alignment Scores:
Pred. No.: 7.87e-64 Length: 1542
Score: 476.00 Matches: 89
Percent Similarity: 95.92% Conservative: 5
Best Local Similarity: 90.82% Mismatches: 4
Query Match: 92.07% Indels: 0
Gaps: 0

US-10-001-254-6 (1-98) x US-09-759-595-4 (1-1542)

Qy 1 ThrtYrValArgCySleuAsnValGlyLeuileArglySleuSerAaspPheileaspPro 20
Db 187 ACATACATACGCAACCTTAATGTGGGATCCTTAGAGAGCTGTGCGATTATTATGATCCT 246
Qy 21 GlnGluGlyTTPlySlySleuAlaValAlaIlelySlyProSerGlyAaspAargTyr 40
Db 247 CAAGAGGGGTGAGAGAAATTAGCAAGTACATCAAAAAGCCGTCGGCGACGACAGATAC 306
Qy 41 AsnGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnThrGlylySseProThSer 60
Db 307 AATCAGTTCATATTAAGAGATTGCAACCTTACTTCAGACCGGAGAGAGCCCACTCTGT 366
Qy 61 GluLeuLeuPheAspTTPGlyThrThraSncYsthrValGlyAapLeuValAspLeuLeu 80
Db 367 GAACCTGCTTTGACTGGGGGACCAAGACTGACAGAGTGGCGACTTGTGATCTACTG 426
Qy 81 IleGlnAsnGlnPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
Db 427 GTCCAGATTGAGCTGTTGGCCCGGACACTCTCGGCTGGCGGATGCGTTCCC 480

RESULT 10
US-09-833-790-149
; Sequence 149, Application US/09833790
; Patent No. US20020068288A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Secrist, Heather
; APPLICANT: Mohamath, Radooh
; APPLICANT: Indrias, Carol Y.
; APPLICANT: Fan, Liqun

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;; FILE REFERENCE: 210121.512
;; CURRENT APPLICATION NUMBER: US/09/833,790
;; NUMBER OF SEQ ID NOS: 440
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 149
;; LENGTH: 501
;; TYPE: DNA
;; ORGANISM: Homo sapien
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)..(501)
;; OTHER INFORMATION: n = A,T,C or G
US-09-833-790-149

Alignment Scores:
Pred. No.: 1.21e-54 Length: 501
Score: 413.00 Matches: 93
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 93.00% Mismatches: 4
Query Match: 79.88% Indels: 4
Gaps: 0

US-10-001-254-6 (1-98) x US-09-833-790-149 (1-501)

Qy 1 ThrtYrValArgCySleuAsnValGlyLeuileArglySleuSerAaspPheileaspPro 20
Db 45 ACATATGTGGCGCTGCGCTCAATGTTGAGCTAATTAGGAAGCTGTCAGATTTATGATCCT 104
Qy 21 GlnGluGlyTTPlySlySleuAlaValAlaIlelySlyProSerGlyAaspAargTyr 40
Db 105 CAAGAGAGATGAGAGAGATTAGCTGTGCTATTAAAGACATGTGTGATGATGATAC 164
Qy 41 AsnGln-PheHisIleArgArgPheGlnAlaLeuLeuGlnThrGlylySseProThSe 60
Db 165 AATCAAGTTTCACATTAAGAGATTGAGACTT-CTTCAAGTGAAGAAAAGTCCACTTC 223
Qy 60 rGluLeuLeuPheAspTTP-GlyThrThraSncYsthrValGlyAapLeuValAspLeu 80
Db 224 TTGATCTGCTTTGACTGGGGGCGACCAAAATGGACAGTGGATCTGTGATCTTT 283
Qy 80 euIleGlnAsnGlnPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
Db 284 TGATCCAAATGAATT-TTGTCTCTCGAGCTTTTGTCTCCAGATGCTGTTCC 338

RESULT 11
US-09-966-451-10
; Sequence 10, Application US/09966451
; Publication No. US20030087856A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
; FILE REFERENCE: PUS-0324
; CURRENT APPLICATION NUMBER: US/09/966,451
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 10
; LENGTH: 31000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; APPLICANT: Fan, Liqun

Alignment Scores:
Pred. No.: 1.95e-27 Length: 31000
Score: 256.00 Matches: 49
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.00% Mismatches: 0
Query Match: 49.52% Indels: 0
Gaps: 0

US-10-001-254-6 (1-98) x US-09-966-451-10 (1-31000)

QY 45 ILeArGaRgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSerGluLeuLeuPhe 64
Db 12963 TTAAGAGAGATTGAAGCATTTACTTCAAACTGAAAAAGTCCCACTTCTGAATTACTGTTT 13022

QY 65 AsPTpGlyThrThrsnCystrValGlyAspLeuValAspLeuLeuIleGlnAsnGlu 84
Db 13023 GACTGGGGCACCAAAATTCACAGTTGGTGAATCTTGATGATCTTTCACAAATGAA 13082

QY 85 PhePheAlaProAlaSerLeuLeuPro 94
Db 13083 TTTTTCCTCCTCGAGTCTTTTCCTCCA 13112

RESULT 12
US-10-630-399-10
; Sequence 10, Application US/10630399
; Publication No. US20040019009A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freiler
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESSION
; FILE REFERENCE: RTS-0324
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/966,451
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 10
; LENGTH: 31000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-630-399-10

Alignment Scores:
Pred. No.: 1,956-27 Length: 31000
Score: 256.00 Matches: 49
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.00% Mismatches: 0
Query Match: 49.52% Indels: 0
DB: 16 Gaps: 0

US-10-001-254-6 (1-98) x US-10-630-399-10 (1-31000)

QY 45 ILeArGaRgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSerGluLeuLeuPhe 64
Db 12963 TTAAGAGAGATTGAAGCATTTACTTCAAACTGAAAAAGTCCCACTTCTGAATTACTGTTT 13022

QY 65 AsPTpGlyThrThrsnCystrValGlyAspLeuValAspLeuLeuIleGlnAsnGlu 84
Db 13023 GACTGGGGCACCAAAATTCACAGTTGGTGAATCTTGATGATCTTTCACAAATGAA 13082

QY 85 PhePheAlaProAlaSerLeuLeuPro 94
Db 13083 TTTTTCCTCCTCGAGTCTTTTCCTCCA 13112

RESULT 13
US-10-001-254-25
; Sequence 25, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sug Hyung
; APPLICANT: Roth, Wilfred
; APPLICANT: Steiner-Liwen, Frank
; TITLE OF INVENTION: No. US20030049702A1 Death Domain Proteins
; FILE REFERENCE: P-107 5037
; CURRENT APPLICATION NUMBER: US/10/001,254

CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 211
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(177)
US-10-001-254-25

Alignment Scores:
Pred. No.: 3,956-29 Length: 211
Score: 247.00 Matches: 46
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.78% Indels: 0
DB: 14 Gaps: 0

US-10-001-254-6 (1-98) x US-10-001-254-25 (1-211)

QY 1 ThrTyValaRgCyLeuAsnValGlyLeuIleArGlyLysSerAspPheIleAspPro 20
Db 25 ACATATGCGCGTGGCTCAATGTGGACTTAATGGAACTGTCAGATTTATTTGATCTT 84

QY 21 GlnGlnGlyTrpLysLeuAlaValAlaIleLysProSerGlyAspAspArgTyr 40
Db 85 CAAGAAGATGGAAAGATTGCTGTACTTAAACCATCTGTGATGATGATAC 144

QY 41 AenGlnPheHisIleArg 46
Db 145 AATCAGTTTCACATAGA 162

RESULT 14
US-10-242-535A-26096
; Sequence 26096, Application US/10242535A
; Publication No. US2004001363A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26096
; LENGTH: 470
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-26096

Alignment Scores:
Pred. No.: 1,256-28 Length: 470
Score: 247.00 Matches: 46
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.78% Indels: 0
DB: 16 Gaps: 0

US-10-001-254-6 (1-98) x US-10-242-535A-26096 (1-470)

QY 1 ThrtYrValaIaGySleuAaVaIGlyleuIleArySleuSerAaPheIleAaPPro 20
 |||||
 Db 139 ACATATGCGCGCTCCCTCAATGTTGAGTAAGAGCTGTCAATTTATTGATCCT 198
 QY 21 GInGluGlyTTPlySLySLeuaIaVaIaIlelySLyProSerGlyAaSPaAArgTYr 40
 |||||
 Db 199 CAAGAAGATGGAAGAGTTCCTGCTAGCTATTAACCACTGCTGATGATGATAC 258
 QY 41 AaGInPheHISleArg 46
 |||||
 Db 259 AATCAGTTTCACATAGA 276

RESULT 15

US-10-085-783A-26096
 ; Sequence 26096, Application US/10085783A
 ; Publication No. US20040037841A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ChondroGene Inc.
 ; APPLICANT: Liew, C.C.
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 ; FILE REFERENCE: 4231/2002
 ; CURRENT APPLICATION NUMBER: US/10/085,783A
 ; CURRENT FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/305,340
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: US 60/275,017
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: US 60/271,955
 ; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 58994
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 26096
 ; LENGTH: 470
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-10-085-783A-26096

Alignment Scores:
 Pred. No.: 1.25e-28 Length: 470
 Score: 247.00 Matches: 46
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 47.78% Indels: 0
 DB: 16 Gaps: 0

US-10-001-254-6 (1-98) x US-10-085-783A-26096 (1-470)

QY 1 ThrtYrValaIaGySleuAaVaIGlyleuIleArySleuSerAaPheIleAaPPro 20
 |||||
 Db 139 ACATATGCGCGCTCCCTCAATGTTGAGTAAGAGCTGTCAATTTATTGATCCT 198
 QY 21 GInGluGlyTTPlySLySLeuaIaVaIaIlelySLyProSerGlyAaSPaAArgTYr 40
 |||||
 Db 199 CAAGAAGATGGAAGAGTTCCTGCTAGCTATTAACCACTGCTGATGATGATAC 258
 QY 41 AaGInPheHISleArg 46
 |||||
 Db 259 AATCAGTTTCACATAGA 276

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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 12, 2005, 05:39:30 ; Search time 412 Seconds
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1248.649 Million cell updates/sec

Title: US-10-001-254-6

Perfect score: 517
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 413486 seque, 2624710521 residues

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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=b1bs -START=1 -END=-1 -MATRIX=blosome2 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO_MMAP -LARGEODERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq_23Sep04.*

1: geneseqn1980s.*
2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002as.*
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8: geneseqn2003as.*
9: geneseqn2003bs.*
10: geneseqn2003cs.*
11: geneseqn2003ds.*
12: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	517 100.0	294 6	AAD40074	Human IRA
2	517 100.0	294 6	AAD59056	Human IRA
3	517 100.0	833 3	AAAO9319	Human can
4	517 100.0	1383 6	AAD40079	Human IRA
5	517 100.0	1383 6	AAD59061	Human IRA
6	517 100.0	1668 5	AAS76805	DNA encod

7	517 100.0	2817 6	AAD40085	Aad40085 Human IRA
8	517 100.0	2817 6	AAD59067	Aad59067 Human IRA
9	517 100.0	2817 10	ACC47548	Acc47548 Human IL-
10	513 99.2	1383 5	AAD10197	Aad10197 Human int
11	476 92.1	1542 5	AAD10198	Aad10198 Mouse int
12	476 92.1	1542 5	AAD10198	Aad10198 Lung smal
13	413 79.9	501 6	AAS61608	Aas61608 Lung smal
14	256 49.5	405 5	AAS76803	Aas76803 DNA encod
15	256 49.5	3100 10	ACC47549	Acc47549 Human DNA
16	247 47.8	211 6	AAD40084	Aad40084 Human IRA
17	247 47.8	211 6	AAD59066	Aad59066 Human IRA
18	247 47.8	415 5	AAS76802	Aas76802 DNA encod
19	247 47.8	2213 3	AAH13798	Aah13798 Human CDN
20	134.5 26.0	408 6	ABO56733	Abg56733 Human KXP
21	96.5 18.7	1791 4	AAF44695	Aaf44695 Novel pro
22	96.5 18.7	1791 12	AD129393	Adi29393 Human MAR
23	96.5 18.7	2277 4	AAO84459	Aac84459 Interleuk
24	96.5 18.7	2288 3	AAZ61602	Aaz61602 DNA encod
25	96.5 18.7	2293 4	AAI57800	Aai57800 Human pol
26	96.5 18.7	2430 5	AAS68902	Aas68902 DNA encod
27	95 18.4	1888 9	ADB61345	Adb61345 CDNA encod
28	84 16.2	1494 5	AAS67194	Aas67194 DNA encod
29	79 15.3	1782 10	AD840440	Ad840440 Human IRA
30	79 15.3	1806 2	AAK77599	Aax77599 Human IRA
31	79 15.3	3459 2	AAK77600	Aax77600 Human IRA
32	78.5 15.2	861 4	AAI37224	Aai37224 Human mus
33	78.5 15.2	861 8	ABX60212	Abx60212 CDNA encod
34	78.5 15.2	861 12	ADJ30962	Adj30962 Human mus
35	78.5 15.2	864 4	AAI37222	Aai37222 Human mus
36	78.5 15.2	864 4	AAI37225	Aai37225 Human mus
37	78.5 15.2	864 8	ABX60213	Abx60213 CDNA encod
38	78.5 15.2	864 8	ABX60210	Abx60210 CDNA encod
39	78.5 15.2	864 12	ADJ30963	Adj30963 Human mus
40	78.5 15.2	864 12	ADJ30960	Adj30960 Human mus
41	77 14.9	756 9	AAD57286	Aad57286 Murine My
42	75.5 14.6	3128 11	ADM02024	Adm02024 Human CDN
43	74.5 14.4	652 6	ABK53369	Abk53369 Human eos
44	74.5 14.4	774 6	ABK73720	Abk73720 Bacillus
45	72.5 14.0	2819 6	ABK52386	Abk52386 DNA encod

ALIGNMENTS

RESULT 1	
AAD40074	standard; CDNA; 294 BP.
AC	AAD40074;
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DT	22-OCT-2002 (first entry)
XX	
DB	Human IRAK4 DD (death domain) cDNA.
XX	
KW	Human; death domain; DD; death effector domain; DED; Chlamydia infection;
KW	NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;
KW	inflammation; allergy; autoimmunity; allograft rejection; cell division;
KW	immune-based pathology; fibrosis; arthritis; graft versus host disease;
KW	Immunosuppressive; gene therapy; anticense therapy; gene; ss.
OS	Homo sapiens.
XX	
PH	Key
FT	CDS
FT	1..294
FT	/*tag= a
FT	/product= "Human IRAK4 DD"
FT	/note= "No start and stop codon"
XX	/partial
XX	
PN	W0200240680-A2.
XX	
PD	23-MAY-2002.
XX	
PF	15-NOV-2001; 2001WO-US044844.

XX 17-NOV-2000; 2000US-00715893.
PR 29-JUN-2001; 2001US-0301889P.
XX

PA (BURN-) BURHAM INST.

PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
PI Stenner-Liewen F;
XX

DR WPI; 2002-500222/53.
DR P-PSDB; AAE24854.

PT New polypeptide comprising a death domain or death effector domain,
PT useful for discovery of drugs that suppress infection, inflammation,
PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.

PS Claim 18; Page 173-174; 209pp; English.

CC The invention relates to an isolated polypeptide comprising a death
CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention
CC is useful for identifying a binding agent, preferably a protein or a drug
CC that binds a DD, DED or NB-ARC domain by contacting a DD, DED or NB-ARC
CC domain from DAP3, IRAK4, CTDP (Chlamydia trachomatis DD protein), DED4 or
CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and
CC detecting the association of the domain and the candidate binding agent,
CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or
CC chemical crosslinking, nuclear magnetic resonance (NMR), mass
CC spectroscopy (MS) and FPA. The invention is useful for modulating the
CC level of a cell process such as cell proliferation, cell adhesion, cell
CC stress responses, responses to microbial infection and B cell
CC immunoglobulin class switching, in particular apoptosis within a cell.
CC Antibody specifically reactive with CTDP DD of C. trachomatis, C.
CC muridarum, C. pneumoniae, and C. pallidum or a nucleic acid encoding the
CC CTDP DD protein is useful for detecting a Chlamydia infection. The
CC invention is useful for modulating the activity of oncogenic proteins,
CC for treating a pathology caused by the oncogenic proteins and for
CC treating bacterial infections by modulating the activity of bacterial
CC proteins. The protein and antibody specific for it are useful for
CC discovery of drugs that suppress infection, inflammation, allergy,
CC sepsis, autoimmunity, allograft rejection and other diseases. The protein
CC is useful for treating immune-based pathologies, pathologies associated
CC with cell division, inflammatory diseases such as sepsis, fibrosis
CC arthritis, graft versus host disease. The invention is used in antisense
CC therapy and gene therapy. The present sequence is human IRAK4 DD cDNA
XX

SO Sequence 294 BP; 84 A; 55 C; 62 G; 93 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,666-64 Length: 294
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-001-254-6 (1-98) X AAD40074 (1-294)

QY 1 ThtTrrValaGqGleuAsnValGlyLeuileAglyLeuSeSaSpheileaspPro 20
Db 1 ACAATATGCGCGCTGCTCAATGTTGACTTAATAGGAAGCTGTCAGATTATATGATCCT 60
QY 21 GInGluGlyTTPLySLyLeuAlaValAlaIleLySLyProSeGlyAspAspArgTy 40
Db 61 CAAGAAGATGGAAGAACTTACCTTACCTTATTAATAAACCACTCGGAGATGATGATAC 120
QY 41 AsnGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnInrGlyLySeSerProThreSer 60
Db 121 AATCAGTTTCACATAGAGAGATTGAGACATTACTTCAACTGAGAAAAGCCCACTTCT 180
QY 61 GluLeuLeuPheAspTrrGlyThThrasnGySthrValGlyAspLeuValAspLeuLeu 80
Db 181 GAATTAATCGTTTGTGACTGGGGGCAACCAAAATGCAAGTGTGATCTTGTGATCTTTTG 240

QY 81 IIGlnAsnGluPhePheAlaProAlaSerLeuLeuProAspAlaValaPro 98
Db 241 ATCCAAAAGAAATTTTGTCTCTCGAGTCTTTTGTCTCCAGATGCTGTTCCC 294

RESULT 2

AAD59056
ID AAD59056 standard; cDNA; 294 BP.

XX AAD59056;

DT 18-DEC-2003 (first entry)

DE Human IRAK4 DD cDNA.

KW Human, death Domain; DD; death effector domain; DED; cell proliferation;
KW Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
KW neural growth factor receptor-interacting death domain; cell adhesion;
KW vasotropic; microbial infection; inflammation; allograft rejection; CTDP;
KW cell stress response; benign prostatic hypertrophy; antibacterial; NIDD;
KW apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
KW neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;
KW keloid; interleukin-1 receptor-associated kinase; IRAK; gene; ss.

OS Homo sapiens.

FH Key Location/Qualifiers
FT CDS 1..294
FT /*tag= a
FT /product= "Human IRAK4 DD protein"
FT /note= "No start and stop codon"
FT /partial

PN US2003049702-A1.

PD 13-MAR-2003.

PF 15-NOV-2001; 2001US-00001254.

PR 17-NOV-2000; 2000US-00715893.

PR 17-NOV-2000; 2000US-0367360P.

PR 29-JUN-2001; 2001US-0301889P.

XX (REED/) REED J C.
PA (GODZ/) GODZIK A.
PA (PAWL/) PAWLOWSKI K.
PA (FIOR/) FIORENTINO L.
PA (LEES/) LEES S H.
PA (ROTH/) ROTH W.
PA (STEN/) STENNER-LIEWEN F.

PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
PI Stenner-Liewen F;
XX

DR WPI; 2002-500222/53.
DR P-PSDB; AAE38897.

PT New polypeptide comprising a death domain or death effector domain,
PT useful for discovery of drugs that suppress infection, inflammation,
PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.

PS Claim 18; Page 33-34; 99pp; English.

CC The present invention provides novel death domain (DD) and death effector
CC domain (DED) proteins and nucleic acids encoding them. The invention also
CC provides death domain containing protein such as Chlamydia trachomatis
CC death domain containing protein (CTDP) DD and neural growth factor
CC receptor-interacting death domain (NIDD) DD. The invention is useful for
CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED
CC or NB-ARC domain from DAP3, IRAK4, CTDP, DED4 or NIDD with a candidate
CC binding agent and identifying an effective agent (e.g. protein or drug)
CC that modulates the association of a DD, DED or NB-ARC domain with protein
CC that binds the DD, DED or NB-ARC domain. The invention is also useful for
CC modulating the level of cell process such as apoptosis, cell adhesion,

CC cell proliferation, cell stress responses, responses to microbial
 CC infection and B cell immunoglobulin class switching, DDE, DDEs and NB-ARC
 CC domains and/or anti-DD, anti-DDE or anti-NB-ARC domain antibodies are
 CC useful for discovery of drugs that suppress infection, autoimmunity,
 CC inflammation, allergy, allograft rejection, sepsis and other diseases.
 CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy,
 CC autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte
 CC hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,
 CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries
 CC following balloon angioplasty (restenosis). The invention is also used in
 CC antibody therapy and gene therapy. The present sequence is human
 CC interleukin-1 receptor-associated kinase (IRAK)-4 DD CDNA

XX SQ Sequence 294 BP; 84 A; 55 C; 62 G; 93 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,66e-64 Length: 294
 Score: 517.00 Matches: 98
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-10-001-254-6 (1-98) x AAD59056 (1-294)

QY 1 ThrTyrValArgCysLeuAenValGlyLeuIleArgLysLeuSerAppheilleaspPro 20
 DB 1 ACATATGTGGCTGCTCCCAATGTGGACTAATTAGAGAGCTGTCAAGTTATTATGATCCT 60
 QY 21 GlnGlnGlyTTPylsLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
 DB 61 CAGAAAGATGAGAAAGATTAGCTGTAGCTATTAAAAACATCTGTGTGATGATAGATAC 120
 QY 41 AsnGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnThrGlyLysSerProThSer 60
 DB 121 AATCAGTTTCACATTAAGAGATTGAAGCACTTACTCAAACTGAAAAAGTCCCATCTCT 180
 QY 61 GluLeuLeuPheAspTTPGlyTThrThrAsnCysThrValGlyAspLeuValAspLeu 80
 DB 181 GAATTACTGTTTGACTGGGACCAACAATTGACAGTGTGTGATCTTGTGATCTTTTG 240
 QY 81 IleGlnAsnGlnPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
 DB 241 ATCCAAATGAATTTTGTCTCCGAGTCTTTTGTCTCCAGATGCTGTTCCC 294

RESULT 3
 AAA09319 standard; DNA; 833 BP.

XX AC AAA09319;

DT 10-AUG-2000 (first entry)

XX Human cancer associated antigen precursor DNA, clone NY-REN-64.

XX renal cancer; cancer associated antigen precursor; diagnosis; cytostatic;

KM 88.

XX Homo sapiens.

OS Key Location/Qualifiers

FT CDS 50..670

PT /tag= a

XX WO200020587-A2.

XX 13-APR-2000.

XX 04-OCT-1999; 99WO-US022873.

XX 05-OCT-1998; 98US-00166300.

XX 05-OCT-1998; 98US-00166350.

PA (LUDW-) LUDWIG INST CANCER RES.

XX Obata Y, Gout I, Tureci O, Sahin U, Pfeundschnuh M, Scanlan MJ;
 PI Stockert E, Chen Y, Old LJ, Jager E, Knuth A;

XX WPI; 2000-303774/26.
 DR P-PSDB; AAY92347.

PT Preventing, diagnosing and/or treating disorders associated with abnormal
 PT expression of human cancer associated antigens.

XX Claim 57; Page 85; 121pp; English.

XX AAA09310-20 are novel genes isolated by SEREX screening from a renal
 CC cancer cell line 1973/10.4. The genes encode cancer associated antigen
 CC precursors. These gene products are useful in methods for preventing,
 CC diagnosing and/or treating disorders, especially cancer, associated with
 CC abnormal expression of human cancer associated antigens. The method
 CC comprises contacting a sample from a subject with an agent that
 CC specifically binds to the nucleic acid molecule or expression product (or
 CC fragment) complexed with a human leukocyte antigen (HLA) molecule and
 CC determining the interaction between the agent and the nucleic acid
 CC molecule or the expression product as a determination of the disorder

XX SQ Sequence 833 BP; 273 A; 155 C; 179 G; 226 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.14e-63 Length: 833
 Score: 517.00 Matches: 98
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-10-001-254-6 (1-98) x AAA09319 (1-833)

QY 1 ThrTyrValArgCysLeuAenValGlyLeuIleArgLysLeuSerAppheilleaspPro 20
 DB 74 ACATATGTGGCTGCTCCCAATGTGGACTAATTAGAGAGCTGTCAAGTTATTATGATCCT 133
 QY 21 GlnGlnGlyTTPylsLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
 DB 134 CAGAAAGATGAGAAAGATTAGCTGTAGCTATTAAAAACATCTGTGTGATGATAGATAC 193
 QY 41 AsnGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnThrGlyLysSerProThSer 60
 DB 194 AATCAGTTTCACATTAAGAGATTGAAGCACTTACTCAAACTGAAAAAGTCCCATCTCT 253
 QY 61 GluLeuLeuPheAspTTPGlyTThrThrAsnCysThrValGlyAspLeuValAspLeu 80
 DB 254 GAATTACTGTTTGACTGGGACCAACAATTGACAGTGTGTGATCTTGTGATCTTTTG 313
 QY 81 IleGlnAsnGlnPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
 DB 314 ATCCAAATGAATTTTGTCTCCGAGTCTTTTGTCTCCAGATGCTGTTCCC 367

RESULT 4

AAD40079 standard; DNA; 1383 BP.

XX AAD40079;

DT 22-OCT-2002 (first entry)

XX Human IRAK4 gene #1.

XX Human; death domain; DD; death effector domain; DED; Chlamydia infection;
 KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;
 KW inflammation; allergy; autoimmunity; allograft rejection; cell division;
 KW immune-based pathology; fibrosis; arthritis; graft versus host disease;
 KW immunosuppressive; gene therapy; antisense therapy; gene; ds.

KM 88.

XX Homo sapiens.

OS

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XX Key Location/Qualifiers
FH CDS 1..1383
FT /tag= a
FT /product= "Human IRAK4"
PN WO200240680-A2.
XX
XX 23-MAY-2002.
XX
XX 15-NOV-2001; 2001MO-US044844.
XX
XX 17-NOV-2000; 2000US-00715893.
XX
XX 29-JUN-2001; 2001US-0301889P.
XX
XX (BURN-) BURHAM INST.
XX
XX Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
XX Stenmer-Liawen F;
XX WPI; 2002-500222/53.
XX
XX P-PSDB; AAE24859.
XX
XX New polypeptide comprising a death domain or death effector domain,
XX useful for discovery of drugs that suppress infection, inflammation,
XX allergy, sepsis, autoimmunity, allograft rejection and other diseases.
XX
XX Claim 19; Page 180-182; 209pp; English.
XX
XX The invention relates to an isolated polypeptide comprising a death
XX domain (DD), death effector domain (DED) or NB-ARC domain. The invention
XX is useful for identifying a binding agent, preferably a protein or a drug
XX that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC
XX domain from DP3, IRAK4, CTDD (Chlamydia trachomatis DP protein), DED4 or
XX NIDD (NGFR-interacting Death Domain), with a candidate binding agent and
XX detecting the association of the domain and the candidate binding agent and
XX by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or
XX chemical crosslinking, nuclear magnetic resonance (NMR), mass
XX spectroscopy (MS) and FPA. The invention is useful for modulating the
XX level of a cell process such as cell proliferation, cell adhesion, cell
XX stress responses, responses to microbial infection and B cell
XX immunoglobulin class switching, in particular apoptosis within a cell.
XX Antibody specifically reactive with CTDD DD of C. trachomatis, C.
XX muridarum, C. pneumoniae, and C. piteacti or a nucleic acid encoding the
XX CTDD DD protein is useful for detecting a Chlamydia infection. The
XX invention is useful for modulating the activity of oncogenic proteins,
XX for treating a pathology caused by the oncogenic proteins and for
XX treating bacterial infections by modulating the activity of bacterial
XX proteins. The protein and antibody specific for it are useful for
XX discovery of drugs that suppress infection, inflammation, allergy,
XX sepsis, autoimmunity, allograft rejection and other diseases. The protein
XX is useful for treating immune-based pathologies, pathologies associated
XX with cell division, inflammatory diseases such as sepsis, fibrosis,
XX arthritis, graft versus host disease. The invention is used in antisense
XX therapy and gene therapy. The present sequence is human IRAK4 gene
XX
XX Sequence 1383 BP; 463 A; 243 C; 283 G; 394 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No: 2,31e-63 Length: 1383
XX Score: 517.00 Matches: 98
XX Percent Similarity: 100.00% Conservat: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: Gaps: 0
XX
XX US-10-001-254-6 (1-98) x AAD40079 (1-1383)
XX
XX QY 1 ThrTyrValArgGyCysLeuAsnValGlyLeuLeuLeuSerAspPheIleAspPro 20
XX Db 25 ACAATATGCGCGCTGCTCAATGTTGAGCTAATTAGAGAGCTGTCAGATTATTCATCCT 84
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XX QY 21 GlnGlnGlyTyrTlySLysLeuAlaValAlaIleSLysProSerGlyAspAspArgTyr 40

```

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XX Db 85 CAGAGAGATGAGAGAGAGTACCTGCTAGCTATTAAAAACATCTGGATAGATATAC 144
XX
XX QY 41 AasnGlnPheHisIleArgArgPheGlnIleuLeuGlnIntnGlyLysSerProThrSer 60
XX Db 145 AATCATTTCACATTAAGAGATTTTGAAGCATTTACTTCAACCTGAGAAAAAGCCACATTC 204
XX
XX QY 61 GlnLeuLeuPheAspTyrTlyThrThrAsnGlyValGlyAspLeuValAspLeuLeu 80
XX Db 205 GAATTACTGTTGACTGGGGGACACAAATGACAGTTGGTGAATCTTGATCTTTTG 264
XX
XX QY 81 IleGlnAsnGlnPhePheAlaProIleSerLeuLeuLeuProAlaValAlaPro 98
XX Db 265 ATCCAAATGAATTTTGTCTCTCGAGCTCTTTGCTCCAGATGCTGTTC 318
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XX RESULT 5
XX AAD59061
XX ID AAD59061 standard; cDNA; 1383 BP.
XX
XX AC AAD59061;
XX
XX DT 18-DEC-2003 (first entry)
XX
XX DE Human IRAK4 full length gene #1.
XX
XX KW Human; death Domain; DD; death effector domain; DED; cell proliferation;
XX Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
XX neural growth factor receptor-interacting death domain; cell adhesion;
XX vasotropic; microbial infection; inflammation; allograft rejection; CTDD;
XX cell stress response; benign prostatic hypertrophy; antibacterial; NIDD;
XX apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
XX neoplasia; restenosis; immunosuppressive; antibody therapy; cytotoxic;
XX keloid; interleukin-1 receptor-associated kinase; IRAK; gene; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT CDS 1..1383
XX FT /tag= a
XX FT /product= "Human IRAK4 protein"
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XX PN US2003049702-A1.
XX
XX XX 13-MAR-2003.
XX PD 15-NOV-2001; 2001US-00001254.
XX PF 17-NOV-2000; 2000US-00715893.
XX PR 17-NOV-2000; 2000US-0367360P.
XX PR 29-JUN-2001; 2001US-0301889P.
XX
XX PA (REED/) REED J C.
XX PA (GODZIK/) GODZIK A.
XX PA (PAWL/) PAWLOWSKI K.
XX PA (FIOR/) FIORENTINO L.
XX PA (LEES/) LEE S H.
XX PA (ROTH/) ROTH W.
XX PA (STEN/) STENMER-LIEWEN F.
XX
XX PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
XX PI Stenmer-Liawen F;
XX
XX DR WPI; 2002-500222/53.
XX DR P-PSDB; AAE38902.
XX
XX PT New polypeptide comprising a death domain or death effector domain,
XX useful for discovery of drugs that suppress infection, inflammation,
XX allergy, sepsis, autoimmunity, allograft rejection and other diseases.
XX
XX Claim 19; Fig 10A; 99pp; English.
XX
XX The present invention provides novel death domain (DD) and death effector
XX domain (DED) proteins and nucleic acids encoding them. The invention also

```

CC provides death domain containing protein such as Chlamydia trachomatis
CC death domain containing protein (CTPD) DD and neural growth factor
CC receptor-interacting death domain (NIDD) DD. The invention is useful for
CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED
CC or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate
CC binding agent and identifying an effective agent (e.g. protein or drug)
CC that modulates the association of a DD, DED or NB-ARC domain with protein
CC that binds the DD, DED or NB-ARC domain. The invention is also useful for
CC modulating the level of cell process such as apoptosis, cell adhesion,
CC cell proliferation, cell stress responses, responses to microbial
CC infection and B cell immunoglobulin class switching. DDEs and NB-ARC
CC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are
CC useful for discovery of drugs that suppress infection, autoimmunity,
CC inflammation, allergy, allograft rejection, sepsis and other diseases.
CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy,
CC autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte
CC hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,
CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries
CC following balloon angioplasty (restenosis). The invention is also used in
CC antibody therapy and gene therapy. The present sequence is human
CC Interleukin-1 receptor-associated kinase (IRAK)-4 full length gene
XX

Sequence 1383 BP; 463 A; 243 C; 283 G; 394 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,31e-63 Length: 1383
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-001-254-6 (1-98) x AAD5961 (1-1383)

QY 1 ThrTyrValArgCysLeuAenValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20
DB 25 ACATATGTGGCTGCTCCCAATGTTGACACTAATTGGAAGCTGTGAGATTATTGACCT 84
QY 21 GlnGlnGlyTTPyLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
DB 85 CAAGAAAGATGAAGAAGATTAGCTGTATTAATAAACATCTGGATGATAGATAC 144
QY 41 AsnGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnInrGlyLysSerProThSer 60
DB 145 AATCAGTTTCACTAAGAGATTGAAAGCATTTCTTCAAACTGAAAAAGTCCCATCTCT 204
QY 61 GluLeuLeuPheAspTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
DB 205 GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTGTGATCTTGGATCTTTTG 264
QY 81 IleGlnAsnGlnPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
DB 265 ATCCAAATGAAATTTTGTCTGCGAGCTTTTGTCTCCCAAGTGTCTCC 318

RESULT 6

AAS76805 standard; cDNA; 1668 BP.

XX AAS76805;

XX 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #12609.

XX Human chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX MO200175067-A2.

XX PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
PA
XX
XX Dmanac RT, Liu C, Tang YT;
PI
XX
XX WPI; 2001-639362/73.
DR P-PSDB; ABG12618.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

Claim 1; SEQ ID NO 12609; 103bp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIFO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 1668 BP; 571 A; 289 C; 332 G; 476 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,99e-63 Length: 1668
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-001-254-6 (1-98) x AAS76805 (1-1668)

QY 1 ThrTyrValArgCysLeuAenValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20
DB 25 ACATATGTGGCTGCTCCCAATGTTGACACTAATTGGAAGCTGTGAGATTATTGACCT 84
QY 21 GlnGlnGlyTTPyLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
DB 85 CAAGAAAGATGAAGAAGATTAGCTGTATTAATAAACATCTGGATGATAGATAC 144
QY 41 AsnGlnPheHisIleArgArgPheGlnAlaLeuLeuGlnInrGlyLysSerProThSer 60
DB 145 AATCAGTTTCACTAAGAGATTGAAAGCATTTCTTCAAACTGAAAAAGTCCCATCTCT 204
QY 61 GluLeuLeuPheAspTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
DB 205 GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTGTGATCTTGGATCTTTTG 264
QY 81 IleGlnAsnGlnPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
DB 265 ATCCAAATGAAATTTTGTCTGCGAGCTTTTGTCTCCCAAGTGTCTCC 318

PA (ROTH/) ROTH W.
 PA (STEN/) STENNER-LIEWEN F.
 XX Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W,
 PI Stenner-Liewen F;
 XX WPI: 2002-500222/53.
 DR P-PSDB: AAE38908.
 XX
 XX New polypeptide comprising a death domain or death effector domain,
 PT useful for discovery of drugs that suppress infection, inflammation,
 PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
 XX
 PS Claim 18; Page 51-53; 99pp; English.
 XX
 CC The present invention provides novel death Domain (DD) and death effector
 CC domain (DED) proteins and nucleic acids encoding them. The invention also
 CC provides death domain containing protein such as Chlamydia trachomatis
 CC death domain containing protein (CTDD) DD and neural growth factor
 CC receptor-interacting protein (CTDD) DD. The invention is useful for
 CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED
 CC or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NID2 with a candidate
 CC binding agent and identifying an effective agent (e.g. protein or drug)
 CC that modulates the association of a DD, DED or NB-ARC domain with protein
 CC that binds the DD, DED or NB-ARC domain. The invention is also useful for
 CC modulating the level of cell process such as apoptosis, cell adhesion,
 CC cell proliferation, cell stress responses, responses to microbial
 CC infection and B cell immunoglobulin class switching. DEDs, DEDs and NB-ARC
 CC domains and/or anti-DD, anti-DD or anti-NB-ARC domain antibodies are
 CC useful for discovery of drugs that suppress infection, autoimmunity,
 CC inflammation, allergy, allograft rejection, sepsis and other diseases.
 CC DD or NB-ARC domain proteins are used to treat infection, allergy,
 CC autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte
 CC hyperplasia, neoplasia, keloid, benign prostatic hyperplasia, fibrosis,
 CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries
 CC following balloon angioplasty (restenosis). The invention is also used in
 CC antibody therapy and gene therapy. The present sequence is human
 CC interleukin-1 receptor-associated kinase (IRAK)-4 full length gene
 XX
 SQ Sequence 2817 BP; 912 A; 547 C; 586 G; 772 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6,22e-63 Length: 2817
 Score: 517.00 Matches: 98
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-10-001-254-6 (1-98) x AAD59067 (1-2817)
 QY 1 ThrTyrValArgCySLeuAsnValGlyLeuIleArgIysLeuSerAspPheIleAspPro 20
 DB 74 ACATATGTGGCGCTCCCTCAATGTTGACTAATTAAGAAAGCTGCTGATTTATGATCCT 133
 QY 21 GlnGluGlyTrpLysLeuAlaValAlaIleLysIleProSerGlyAspAspArgTyr 40
 DB 134 CAAGAAGAGATGAAGAAAGTGTAGCTGATTAATAAACAATCTGGTGATGATGATAC 193
 QY 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnTrpGlyLysSerProThrSer 60
 DB 194 AATCAGTTTCACATRAGAGATTGAGACATTACTTCAATCGAAGAAAGCCCACTTCT 253
 QY 61 GluLeuLeuPheAspTrpGlyThrThrAsnCyThrValGlyAspLeuValAspLeu 80
 DB 254 GAATTACTGTTTGATGGGACCAACAATTGACAGTTGGTGTATCTTGATCTTTTG 313
 QY 81 IlleGlnAsnGluPhePheAlaProAlaSerLeuLeuPheProAlaValPro 98
 DB 314 ATCCAAATGAATTTTGTCTCTGGAGCTCTTGTCTCCAGATGCTGTCC 367
 RESULT 9
 ACC47548

ID ACC47548 standard; DNA; 2817 BP.
 XX
 AC ACC47548;
 XX
 DT 11-JUL-2003 (first entry)
 XX
 DE Human IL-1 receptor-associated kinase-4 sequence # SEQ ID 3.
 XX
 XX Antisense therapy; cytostatic; antimicrobial; antiinflammatory;
 KM interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer;
 KM inflammatory disease; infection; diagnostic; therapeutic; prophylaxis;
 XX gene; ds.
 XX
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 50..1432
 FT /*tag= a
 FT /product= "IL-1 receptor-associated kinase-4"
 XX
 FM MO2003028636-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 26-SEP-2002; 2002MO-US030574.
 XX
 PR 28-SEP-2001; 2001US-00966451.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett FC, Freiler SM;
 XX
 DR WPI: 2003-363256/34.
 DR P-PSDB: ABR44401.
 XX
 XX New antisense oligonucleotides for modulating IL-1 receptor-associated
 PT kinase-4 gene expression, particularly useful for preventing, delaying or
 PT treating e.g. cancer (e.g. renal cancer), inflammatory disease or an
 PT infection.
 XX
 PS Example 13; Page 80-83; 119pp; English.
 XX
 CC The invention relates to a compound of 8-50 nucleobases which is targeted
 CC to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated
 CC kinase-4, specifically hybridizing with the nucleic acid and inhibiting
 CC the expression of the encoded product. Also disclosed is the compound
 CC hybridizing with an 8-nucleobase portion of an active site on a nucleic
 CC acid molecule encoding IL-1 receptor-associated kinase-4. The antisense
 CC oligonucleotide is useful for treating an animal having a disease or
 CC conditions associated with IL-1 receptor-associated kinase-4, e.g. cancer
 CC (particularly renal cancer), inflammatory disease or an infection. The
 CC antisense compounds are useful for diagnostics, therapeutics,
 CC prophylaxis, or as research reagents or kits. The current sequence
 CC represents the human IL-1 receptor-associated kinase-4 encoding sequence
 CC (GenBank accession number NM_016123)
 XX
 SQ Sequence 2817 BP; 912 A; 547 C; 586 G; 772 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6,22e-63 Length: 2817
 Score: 517.00 Matches: 98
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-10-001-254-6 (1-98) x ACC47548 (1-2817)
 QY 1 ThrTyrValArgCySLeuAsnValGlyLeuIleArgIysLeuSerAspPheIleAspPro 20
 DB 74 ACATATGTGGCGCTCCCTCAATGTTGACTAATTAAGAAAGCTGCTGATTTATGATCCT 133
 QY 21 GlnGluGlyTrpLysLeuAlaValAlaIleLysIleProSerGlyAspAspArgTyr 40

Dd		133	CAGAAGGATGGAAAGTAGCTGTAGTATTAAAAACATCGTGAGTANAGTATAC	197
Oy		41	AAGnGlnPheHisIleArgArgPheGluAlaLeuLenuInrHrgLylySerProThSer	60
Dd		194	AATCAgTTTCACATAAGGAATTTGAAGCATTACTTCAACTGAAAAGGCCACATCTC	253
Oy		61	GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu	80
Dd		254	GAATTAAGTCTGTTTACTGCGGCACACACAATTGCAAGTGGTGTATCTTGAGATCTTTG	313
Oy		81	IleGlnAsnGlnPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro	98
Dd		314	ATCCAAAAGAAATTTTTTGTCTCTCGAGTCCTTTTGCTCCAGATGCTGTTCCC	367
RESULT 10				
AAD10197				
ID	AAD10197	standard; cDNA; 1383 bp.		
XX				
AC	AAD10197;			
XX				
DT	24-SEP-2001	(first entry)		
DE				
XX				
Human	interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 cDNA.			
KW	Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytosolic;			
KM	IL; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD;			
KW	chronic obstructive pulmonary disease; neutroprotective; chronic cough;			
KV	adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS;			
KW	interstitial lung disease; allergic rhinitis; transplant rejection;			
KW	autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;			
KV	multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke;			
KW	cardiovascular disease; atherosclerosis; neurodegenerative disease;			
KV	sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis;			
KW	inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis;			
KV	Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor;			
KW	sarcoidosis; transgenic animal; ss.			
XX				
OS	Homo sapiens.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	1..1383		
FT		/*tag= a		
FT		/product= "Human IRAK-4"		
PX	WO200151641-A1.			
PN				
XX				
PD	19-JUL-2001.			
XX				
PF	12-JAN-2001; 2001WO-US001171.			
XX				
PR	13-JAN-2000; 2000US-0176395P.			
XX				
PA	(TULA-) TULARIX INC.			
PI				
XX	Weesche H, Li S;			
XX	WPI; 2001-451860/48.			
DR	P-PSDB; AAE05398.			
PT				
Novel	human interleukin-1 receptor associated kinase polypeptide, useful			
for	identifying modulators of the polypeptide for treating gout, asthma,			
allergic	rhinitis, multiple sclerosis and skin cancer.			
Claim	7; Fig 2; 8pp; English.			
The	present sequence is a cDNA encoding human interleukin (IL)-1 receptor			
associated	kinase (IRAK)-4. IRAK associate with activated IL-1, IL-18 and			
other	receptors and act to transduce signals originating from the			
activated	receptors, ultimately leading to a variety of downstream			
effects	such as nuclear factor (NF)-kappaB activation. The IRAK-4			
inhibitors	are useful for treating inflammatory diseases such as			
pulmonary	diseases and diseases of the airway [e.g., adult respiratory			

CC	diseases fibrosis (ARDS), chronic obstructive pulmonary disease (COPD),
CC	pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or
CC	allergic rhinitis), transplant rejection, autoimmune diseases (e.g.,
CC	rheumatoid arthritis), systemic lupus erythematosus, multiple sclerosis or
CC	diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma),
CC	cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of
CC	the central nervous system (e.g., neurodegenerative disease), CD4
CC	mediated sepsis, non-CD4 mediated sepsis, osteoarthritis, osteoporosis,
CC	psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic
CC	dermatitis), inflammatory bowel disease (e.g., Crohn's disease and
CC	ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout,
CC	sarcoidosis and ophthalmic diseases and conditions. The inhibitors of
CC	IRAK-4 activity or expression are used to inhibit signal transduction
CC	resulting from the activation of an interleukin-1 receptor (IL-1R)/Toll
CC	receptor in a cell. They also inhibit the activation of a transcription
CC	factor that activates NF-kappaB in the cell. IRAK-4 is used to create a
CC	nonhuman transgenic animal which is useful for testing the function of
CC	IRAK-4 in vivo, to generate models for the study of inflammatory
CC	disorders and conditions and for the development of potential treatments
CC	for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences
CC	are also used in gene therapy and in antisense therapy
xx	
xx	
SQ	Sequence 1383 BP; 463 A; 244 C; 283 G; 393 T; 0 U; 0 Other;
	Alignment Scores:
Pred. No.:	8,59e-63 Length: 1383
Score:	513.00 Matches: 97
Percent Similarity:	98.98% Conservative: 0
Best Local Similarity:	98.98% Mismatches: 1
Query Match:	99.23% Indels: 0
DB:	5 Gaps: 0
US-10-001-254-6 (1-98) x AAD10197 (1-1383)	
OY	1 Thr-Ty-ValArg-CysLeuAsnValGlyIleuLeIeArgLysLeuSerAapPheIIeaSPPro 20
Db	25 ACATATGTGGCGCTCAATTGGACTTTGACATAATTAGAAAGCTGTACGATTTTAITGATCCT 84
OY	21 GlnglGngLTTPriyAlsyLeuNlaValAlaIleuYlsyPSroSGIyaSPasparTyR 40
Db	85 CAAGAAGAGTAGGAAGAAAGTTAGCTGTACCTGATCAAATAAACATCTGGTGATGATAGATAC 144
OY	41 AsnGlPhaHsiIlekrGrphgeglunAlaleuengInmrngLylyrSsrProThSer 60
Db	145 AAACAAGTTTCACATTAAGAGATTTAAGCATTTACTTCAATGTGAAGAAAGGCCCACTTCT 204
OY	61 GluLeuLeuPheaSPTrIpclYThrThraAnCySThrValGIyaSPLeuValaSPLeuLeu 80
Db	205 GAATTACTGTGTGACGTGGGGCACCAAAATTGCACAGCTGGTGATCTTGIGATCTTTTG 264
OY	81 IlleglAnsglnPhphealArProLaaserLeuLeuPProApAlaValPro 98
Db	265 ATCCAATAAGAAATTTTTTGTCTTCGCGAGCTCTTTTGCTCCCAATGCTGTTCCTC 318
RESULT 11	
AAD10198	
ID	AAD10198 standard, cDNA; 1542 BP.
XX	
XX	AAD10198;
AC	
DT	24-SEP-2001 (first entry)
XX	
XX	Mouse interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 cDNA.
KW	Mouse; interleukin-1 receptor associated kinase-4; IRAK-4; cytosolic;
KW	IL; antibacterial; anti-inflammatory; ophthalmological; vasotropic; OPD;
KW	chronic obstructive pulmonary disease; neuroprotective; chronic cough;
KW	adult respiratory disease syndromes; pulmonary fibrosis; asthma; ARDS;
KW	interstitial lung disease; allergic rhinitis; transplant rejection;
KW	autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
KW	multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke;
KW	cardiovascular disease; atherosclerosis; neurodegenerative disease;
KW	sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis;

KW inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis;
 KM Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor;
 XX sarcoidosis; transgenic animal; ss.
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1542 /*tag= a
 FT /product= "Mouse IRAK-4"
 XX
 PN W0200151641-A1.
 XX
 PD 19-JUL-2001.
 XX
 PF 12-JAN-2001; 2001WO-US001171.
 XX
 PR 13-JAN-2000; 2000US-0176395P.
 XX
 PA (TUL-) TULARIK INC.
 XX
 PI Mesche H, Li S;
 XX
 DR WPI; 2001-451860/48.
 DR P-PSDB; AAE05399.
 XX
 PT Novel human interleukin-1 receptor associated kinase polypeptide, useful
 PT for identifying modulators of the polypeptide for treating gout, asthma,
 PT allergic rhinitis, multiple sclerosis and skin cancer.
 XX
 PS Claim 26; Fig 4; 89pp; English.
 XX
 CC The present sequence is a cDNA encoding mouse interleukin (IL)-1 receptor
 CC associated kinase (IRAK)-4. IRAK associate with activated IL-1, IL-18 and
 CC other receptors and act to transduce signals originating from the
 CC activated receptors, ultimately leading to a variety of downstream
 CC effects such as nuclear factor (NF)-kappa activation. The IRAK-4
 CC inhibitors are useful for treating inflammatory diseases such as
 CC pulmonary diseases and diseases of the airway (e.g., adult respiratory
 CC disease syndrome (ARDS), chronic obstructive pulmonary disease (COPD),
 CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or
 CC allergic rhinitis), transplant rejection, autoimmune diseases (e.g.,
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or
 CC diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma),
 CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of
 CC the central nervous system (e.g., neurodegenerative disease), CD14
 CC mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis,
 CC psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic
 CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and
 CC ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout,
 CC sarcoidosis and ophthalmic diseases and conditions. The inhibitors of
 CC IRAK-4 activity or expression are used to inhibit signal transduction
 CC resulting from the activation of an interleukin-1 receptor (IL-1R)/Toll
 CC receptor in a cell. They also inhibit the activation of a transcription
 CC factor that activates NFkappaB in the cell. IRAK-4 is used to create a
 CC nonhuman transgenic animal which is useful for testing the function of
 CC IRAK-4 in vivo, to generate models for the study of inflammatory
 CC disorders and conditions and for the development of potential treatments
 CC for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences
 CC are also used in gene therapy and in antisense therapy
 XX
 SQ Sequence 1542 BP; 421 A; 392 C; 423 G; 306 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.93e-57 Length: 1542
 Score: 476.00 Matches: 89
 Percent Similarity: 95.92% Conservative: 5
 Best Local Similarity: 90.82% Mismatches: 4
 Query Match: 92.07% Indels: 0
 DB: 5 Gaps: 0

US-10-001-254-6 (1-98) x AAD10198 (1-1542)

QY 1 ThrTyValArgCysLeuAenValGlyLeuIleArgIysLeuSerAspPheIleAspPro 20
 DB 187 ACATACATACGCAACCTTAATGTGGGGATCCCTTAGAAGCTGTGGATTATTAATGATCCT 246
 QY 21 GlnGluGlyTTPylsYlsLeuAlaValAlaIleIlylsYrsProSerGlyAspAspArgTyr 40
 DB 247 CAAAGAGGGTGGAGAAATTAAGCATAGCTATCAAAAAGCCGTCCGCGACAGACATAC 306
 QY 41 AsnGlnPheHisIleAArgPheGluAlaLeuLeuGlnThrGlyIysSerProThrSer 60
 DB 307 AATCAGTTCATATTAAGAGATTCAGACCTTACTTACAGCCGGAGAGACCCCACTGT 366
 QY 61 GluLeuLeuPheAspIlePylGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
 DB 367 GAACGTGCTGTTTGACTGGGACACAGACCTGACCACTGTGGCCACTTGTGGATCTACTG 426
 QY 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
 DB 427 GTCCAGATTGAGCTGTTTGGCCCCGCCACACTCTCTGCTGGCGGATGCCGTCC 480
 RESULT 12
 ID AAS61608 standard; cDNA; 501 BP.
 XX
 AC AAS61608;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Lung small cell carcinoma antigen, cDNA #149.
 XX
 KM Human; cytostatic; antitumour; lung small cell cancer antigen; tumour;
 KM lung cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200177168-A2.
 PD 18-OCT-2001.
 XX
 PF 11-APR-2001; 2001WO-US011859.
 XX
 PR 11-APR-2000; 2000US-0196780P.
 PR 21-JUN-2000; 2000US-0213361P.
 PR 01-SEP-2000; 2000US-0229763P.
 PR 05-SEP-2000; 2000US-0230629P.
 PR 14-SEP-2000; 2000US-0232565P.
 PR 19-DEC-2000; 2000US-0257037P.
 PR 08-JAN-2001; 2001US-0260796P.
 XX
 PA (CORI-) CORIAX CORP.
 XX
 PI Lodes MJ, Wang T, Mohamath R, Indirias CY;
 XX
 DR WPI; 2002-010896/01.
 XX
 PT Lung tumor polynucleotide and polypeptides useful in therapy and
 PT diagnosis of cancer especially lung cancer.
 XX
 PS Claim 1; Page 174; 295pp; English.
 XX
 CC The invention relates to novel isolated lung small cell cancer antigen
 CC polynucleotides (I) and polypeptides (II) used in a method of detecting
 CC cancer in a patient. The method is optionally performed by utilising
 CC oligonucleotides (III), where the biological sample from the patient is
 CC contacted with (III), detecting the amount of polynucleotide hybridised
 CC to (III) in the sample and comparing the amount of polynucleotide to a
 CC predetermined cut-off value and thereby determining cancer in a patient.
 CC (I), (II) or antigen-presenting cells expressing (II) is useful for
 CC stimulating and/or expanding T cells specific for a tumour protein. The
 CC method comprises contacting T cells with one of the components under
 CC conditions to permit the stimulation and/or expansion of the cells. A
 CC composition comprising (I) is useful for stimulating an immune response
 CC in a patient and for inhibiting the development of a cancer especially

CC lung cancer in a patient. An isolated T cell population is useful for
 CC removing tumor cells from the biological sample and for inhibiting the
 CC development of cancer in a patient. AAS61460-AAS61874 represent novel
 CC human lung small cell cancer antigen coding sequences of the invention
 XX

Sequence 501 BP; 166 A; 102 C; 97 G; 134 T; 0 U; 2 Other;
 Alignment Scores:
 Pred. No.: 4 01e-49 Length: 501
 Score: 413.00 Matches: 93
 Percent Similarity: 94.00% Conservative: 1
 Best Local Similarity: 93.00% Mismatches: 4
 Query Match: 79.88% Indels: 4
 DB: 6 Gaps: 0

US-10-001-254-6 (1-98) x AAS61608 (1-501)

QY 1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAapPro 20
 Db 45 ACATATGTCGCGCTGCCTCAATGTGGACTAATAGGAAGCTGTCAATTTTATGATCCT 104
 QY 21 GlnGluGlyTTPDlyLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
 Db 105 CAAGAAGGATGGAGAAGATTAGCTGTAGCTATTAAAAACCACTGGTATGATGATGATAC 164
 QY 41 AsnGln-PheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThise 60
 Db 165 AATCAAGTTTCACATAGAGAGATTTGACACATT-CTTCAAACTGGAAAAAGTCCCACTTC 223
 QY 60 rGluLeuLeuPheAspTTP-GlyThrThrAsnCysThrValGlyAspLeuValAspLeuL 80
 Db 224 TTGAATACTGTTTGAAGCTGGGGCACCACAAATTGACAGTGGTGTGATCTTGGATCTTT 283
 QY 80 euIleGlnAsnGluPhePheAlaProAlaSerLeuLeuProAlaValPro 98
 Db 284 TGATCCAAATGAAATT-TTGTCTCTCGAGTCTTTTGTCTCCAGAGTGTCTCC 338
 RESULT 13
 AAS76803
 ID AAS76803 standard; cDNA; 405 BP.
 XX
 AC AAS76803;
 XX
 DT 13-FEB-2002 (first entry)
 DE DNA encoding novel human diagnostic protein #12607.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 XX
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI, 2001-639362/73.
 XX
 DR P-PSDB; ABG12616.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX

PS Claim 1; SEQ ID NO 12607; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (II) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/published_pct_sequences

SQ Sequence 405 BP; 93 A; 87 C; 83 G; 142 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 7 96e-27 Length: 405
 Score: 256.00 Matches: 49
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 98.00% Mismatches: 0
 Query Match: 49.52% Indels: 0
 DB: 5 Gaps: 0

US-10-001-254-6 (1-98) x AAS76803 (1-405)

QY 45 IleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSerGlyLeuLeuPhe 64
 Db 114 TTAGGAGATTGAGACATTACTTCAAACTGGAAAAAGTCCCACTTGAATTAAGTCTTT 173
 QY 65 AspTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeuIleGlnAsnGlu 84
 Db 174 GACTGGGGCACCACAAATTGACAGTGGTGTGATCTTGGATCTTGAATCAAAATGAA 233
 QY 85 PhePheAlaProAlaSerLeuLeuPro 94
 Db 234 TTTTGTCTCTCGAGTCTTTGTCTCCCA 263
 RESULT 14
 ACC47549
 ID ACC47549 standard; DNA; 31000 BP.
 XX
 AC ACC47549;
 XX
 DT 11-JUL-2003 (first entry)
 DE Human DNA complement sequence # SEQ ID 10.
 XX
 KW Antisense therapy; cytostatic; antimicrobial; antiinflammatory;
 KW interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer;
 KW inflammatory disease; infection; diagnostic; therapeutic; prophylaxis;
 KW ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003028636-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 26-SEP-2002; 2002WO-US030574.
 XX
 PR 28-SEP-2001; 2001US-00966451.
 XX

PA (ISIS-) ISIS PHARM INC.
XX Bennett FC, Freier SM;
PI WPI; 2003-363256/34.
XX
DR
XX
PT New antisense oligonucleotides for modulating IL-1 receptor-associated
PT kinase-4 gene expression, particularly useful for preventing, delaying or
PT treating e.g. cancer (e.g. renal cancer), inflammatory disease or an
PT infection.
XX
PS Example 15; Page 85-102; 119pp; English.
XX
CC The invention relates to a compound of 8-50 nucleobases which is targeted
CC to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated
CC kinase-4, specifically hybridizing with the nucleic acid and inhibiting
CC the expression of the encoded product. Also disclosed is the compound
CC hybridizing with an 8-nucleobase portion of an active site on a nucleic
CC acid molecule encoding IL-1 receptor-associated kinase-4. The antisense
CC oligonucleotide is useful for treating an animal having a disease or
CC conditions associated with IL-1 receptor-associated kinase-4, e.g. cancer
CC (particularly renal cancer), inflammatory disease or an infection. The
CC antisense compounds are useful for diagnostics, therapeutics,
CC prophylaxis, or as research reagents or kits. The current sequence is
CC utilized in an example from the invention in the design of antisense
CC oligonucleotides, and represents the complement of the human DNA sequence
CC that is given as Genbank accession number AC016143
XX
SQ Sequence 31000 BP; 9247 A; 5856 C; 5924 G; 9973 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 3.38e-24 Length: 31000
Score: 256.00 Matches: 49
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.00% Mismatches: 0
Query Match: 49.52% Indels: 0
DB: Gaps: 10
US-10-001-254-6 (1-98) x ACC47549 (1-31000)
QY 45 IleaRgArpGheGuaIaLeuLeuGlnThrGlySerProThrSerGlnLeuLeuPhe 64
Db 12963 TTAAGAGATTGGAAGATTACTTCAAACTGGAAGAAAGTCCCACTTGGAATTACTGTTT 13022
QY 65 AspTTPGlyThrThrAsnCyThValGlyAspLeuValAspLeuLeuIleGlnAsnGlu 84
Db 13023 GACTGGGCGCACCAAAATGACAGTTGGTGTGATCTTTGATCCAAATGAA 13082
QY 85 PhePheAlaProAlaSerLeuLeuPro 94
Db 13083 TTTTGTCTCTGCGAGCTTTGTCTCCA 13112
RESULT 15
AAD40084
ID AAD40084 standard; DNA; 211 BP.
XX
AC AAD40084;
XX
DT 22-OCT-2002 (first entry)
XX
DE Human IRAK4 short gene.
XX
KW Human; death domain; DD; death effector domain; DED; Chlamydia infection;
KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;
KW inflammation; allergy; autoimmunity; allograft rejection; cell division;
KW immune-based pathology; fibrosis; arthritis; graft versus host disease;
KW immunosuppressive; gene therapy; antisense therapy; gene; de.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 1..180
FT /*tag= a

FT /product= "Human IRAK4 short protein"
XX
XX WO200240680-A2.
XX
XX 23-MAY-2002.
XX
XX 15-NOV-2001; 2001WO-US044844.
XX
XX 17-NOV-2000; 2000US-00715893.
XX
XX 29-JUN-2001; 2001US-0301889P.
XX
XX (BURN-) BURNHAM INST.
XX
XX
XX Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
XX Steiner-Liwen F;
XX WPI; 2002-500222/53.
XX
XX P-PSDB; AAE24864.
XX
XX New polypeptide comprising a death domain or death effector domain,
XX useful for discovery of drugs that suppress infection, inflammation,
XX allergy, sepsis, autoimmunity, allograft rejection and other diseases.
XX
XX Claim 19; Page 195; 209pp; English.
XX
CC The invention relates to an isolated polypeptide comprising a death
CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention
CC is useful for identifying a binding agent, preferably a protein or a drug
CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC
CC domain from DAP3, IRAK4, CTDP (Chlamydia trachomatis DD protein), DED4 or
CC NIND (NGPR-interacting Death Domain), with a candidate binding agent and
CC detecting the association of the domain and the candidate binding agent,
CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or
CC chemical crosslinking, nuclear magnetic resonance (NMR), mass
CC spectroscopy (MS) and FPA. The invention is useful for modulating the
CC level of a cell process such as cell proliferation, cell adhesion, cell
CC stress responses, responses to microbial infection and B cell
CC immunoglobulin class switching, in particular apoptosis within a cell.
CC Antibody specifically reactive with CTDP DD of C. trachomatis, C.
CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the
CC CTDP DD protein is useful for detecting a Chlamydia infection. The
CC invention is useful for modulating the activity of oncogenic proteins,
CC for treating a pathology caused by the oncogenic proteins and for
CC treating bacterial infections by modulating the activity of bacterial
CC proteins. The protein and antibody specific for it are useful for
CC discovery of drugs that suppress infection, inflammation, allergy,
CC sepsis, autoimmunity, allograft rejection and other diseases. The protein
CC is useful for treating immune-based pathologies, pathologies associated
CC with cell division, inflammatory diseases such as sepsis, fibrosis,
CC arthritis, graft versus host disease. The invention is used in antisense
CC therapy and gene therapy. The present sequence is human IRAK4 short gene
XX
SQ Sequence 211 BP; 77 A; 41 C; 36 G; 57 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 6.19e-26 Length: 211
Score: 247.00 Matches: 46
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.78% Indels: 0
DB: Gaps: 0
US-10-001-254-6 (1-98) x AAD40084 (1-211)
QY 1 ThrTyValArgCyLeuAsnValGlyLeuLeuArgTyLeuSerAspPheIleAspPro 20
Db 25 ACATATGGCGCTCCCTCAATGTTGACCTAATTGGAAGCTGTGACTTTTATGATCCT 84
QY 21 GlnGlnGlyTTPblyblyblyblyblyblyblyblyblyblyblyblyblyblyblyblybly 40
Db 85 CAAGAAGAGTGAAGAAGATTGCTGTGCTATTAAAAAACATCTGTGTGATGATGATAC 144
QY 41 AsnGlnPheHisIleArg 46

Db |||||||
 145 AATCAGTTTCACATAAGA 162

Search completed: January 12, 2005, 07:14:08
Job time : 421 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: January 12, 2005, 06:22:23 / Search time 2550 Seconds
(without alignment)
1400.429 Million cell updates/sec

Title: US-10-001-254-6
Perfect score: 517
Sequence: 1 TYVRCINLVGIRKLSDFIDP.....LTIQNEFPAPASLLLPDAPV 98

Scoring table:
BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 segs, 18219865908 residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO.spool_h/US10001254/runat_10012005_172739_10471/app.query.fasta_1.263
-DB=EST -QFMT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10001254 @CGN 1.1 3437 @runat_10012005_172739_10471 -NCPU=6 -ICPU=3
-NO MMAP -LARGESUBSTRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_g981:
9: gb_g982:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	517	100.0	859	4	BG164491 602342026
2	511	98.8	821	7	CK459029 923479 MA
3	509	98.5	811	4	BG616438 602642772
4	495	95.7	402	2	BR482619 168463 BA
5	495	95.7	666	2	CN788062 4122347 B
6	485	93.8	719	2	BR696981 602130160
7	476	92.1	503	6	CA538859 C0272B01-
8	476	92.1	598	5	BO552228 H4014C09-
9	476	92.1	610	2	BB660378 BB660378

10	476	92.1	637	2	BB613447
11	476	92.1	638	6	BY721552
12	476	92.1	663	6	BY726858
13	476	92.1	676	2	BB613167
14	476	92.1	1161	3	AK020397
15	476	92.1	2481	3	AK028837
16	476	92.1	2810	3	AK029028
17	472	91.3	575	5	BX522921
18	450	87.0	1383	9	AY418791
19	443	85.7	1383	9	AY418792
20	430.5	83.3	524	2	AM106160
21	415.5	80.4	1286	2	AY418793
22	415	80.3	541	4	BG691069
23	414.5	80.2	507	2	BB866698
24	393	76.0	453	2	BB866349
25	393	76.0	852	5	BU209111
26	389	75.2	600	1	AJ453616
27	389	75.2	670	1	AJ447581
28	369	71.4	265	2	AM436511
29	359	69.4	686	7	CN066297
30	359	69.4	711	7	CN067840
31	359	69.4	775	7	CN061000
32	359	69.4	782	7	CN064552
33	349	67.5	313	4	BM151935
34	346	66.9	417	7	C0780006
35	343	66.3	606	1	AL647125
36	323.5	62.6	664	4	BU035962
37	319	61.7	479	7	CR370093
38	319	61.7	689	7	CR375297
39	319	61.7	793	5	BR876165
40	310	60.0	599	4	BA691338
41	296	57.3	632	6	CA365604
42	289	55.9	743	6	CA474136
43	289	55.9	815	7	CR866056
44	287	55.5	555	2	AM423082
45	287	55.5	771	7	CN507749

ALIGNMENTS

RESULT 1
BG164491 859 bp mRNA linear EST 06-FEB-2001
LOCUS 602342026F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4452055 5',
DEFINITION mRNA sequence.
ACCESSION BG164491.1 GI:12671194
VERSION BG164491.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 859)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNML Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
http://Image.lnl.gov
Plate: LHAM10240 row: d column: 08
High quality sequence stop: 634.
Location/Qualifiers
1: 859
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4452055"

FEATURES

source

/tissue_type="hypertrophoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 89"
/note="Organ: kidney; Vector: pCMV-SORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	7.9e-60	Length:	859
Score:	517.00	Matches:	98
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-001-254-6 (1-98) x BG164491 (1-859)

QY 1 ThTtYValaTgCySeuAenValGlyLeuIlleArglySeuSerAaspPheIlleAapPro 20
DB 59 ACATATGTCGGCTCCCTCAATGTTGACCTAATTAAGAAAGTGTGATTTTATTGATCTT 118
QY 21 GIngluglYtTPlYslySeuAlaValAllelyslYsProSerGlyAaspAparGtyr 40
DB 119 CAAGAAAGATGGAAGAGATTAGCTGATTAATAAACCATCTGCTGATGATGATAC 178
QY 41 AaNgInPheHsIlleArgPheGluAlaLeuLengInThrGlyLysSerProThrSer 60
DB 179 AATCATTTTCACTAAGAGATTGAAGCACTTCAAACTGAAAAAATCCACACTCT 238
QY 61 GlUleuLeuPheAspTtPglYThrThraSncYsThrValGlyAaspLeuValAaspLeu 80
DB 239 GAATTAAGTCTTGAATGAGGACCAACAATTGACAGTTGATCTTGATCTTTG 298
QY 81 lIeGlnaEnGluPhePheAlaProAlaSerleuLeuProAapAlaValPro 98
DB 299 ATCCAAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTCCC 352

RESULT 2
LOCUS CK459029 821 bp mRNA linear EST 14-JAN-2004
DEFINITION 923479 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION CK459029
VERSION CK459029.1 GI:40830310
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
AUTHORS Smlth,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
Nonneman,D.J., Wray,J.B. and Keeler,J.W.
TITLE Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: TMW8032 row: K column: 23
Seq primer: GTAATACGACCTCATCTATGAGG.
FEATURES
location/Qualifiers
1..821
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"

/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4PIG"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."

ORIGIN

Alignment Scores:

Pred. No.:	4.92e-59	Length:	821
Score:	511.00	Matches:	96
Percent Similarity:	98.98%	Conservative:	1
Best Local Similarity:	97.96%	Mismatches:	0
Query Match:	98.84%	Indels:	0
DB:	7	Gaps:	0

US-10-001-254-6 (1-98) x CK459029 (1-821)

QY 1 ThTtYValaTgCySeuAenValGlyLeuIlleArglySeuSerAaspPheIlleAapPro 20
DB 233 ACATATGTCGGCTCCCTCAATGTTGACCTAATTAAGAAAGTGTGATTTTATTGATCTT 292
QY 21 GIngluglYtTPlYslySeuAlaValAllelyslYsProSerGlyAaspAparGtyr 40
DB 293 CAAGAAAGATGGAAGAGATTAGCTGATTAATAAACCATCTGCTGATGATGATAC 352
QY 41 AaNgInPheHsIlleArgPheGluAlaLeuLengInThrGlyLysSerProThrSer 60
DB 353 AACCATTTTCACTAAGAGATTGAAGCACTTCAAACTGAAAAAAGTCCACACTTGT 412
QY 61 GlUleuLeuPheAspTtPglYThrThraSncYsThrValGlyAaspLeuValAaspLeu 80
DB 413 GAATTAAGTCTTGAATGAGGACCAACAATTGACAGTTGATCTTGATCTTTG 472
QY 81 lIeGlnaEnGluPhePheAlaProAlaSerleuLeuProAapAlaValPro 98
DB 473 GTCCAAAATGAATTTTGTCTCTGCGAGCTTTTGTCTCCAGATGCTGTCCC 526

RESULT 3
LOCUS BG616438 811 bp mRNA linear EST 18-APR-2001
DEFINITION 602642727 NIH MGC_61 Homo sapiens cDNA clone IMAGE:4773760 5',
mRNA sequence.
ACCESSION BG616438
VERSION BG616438.1 GI:13667809
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: ATCC

CNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1645 row: p column: 17
High quality sequence start: 3
High quality sequence stop: 613.
FEATURES
location/Qualifiers
1..811
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4773760"
/tissue_type="embryonal carcinoma"

/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 61"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctggcgc); Site_2: SfiI (ggccatctggcgc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTAGAGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCCGAGCGCCGACATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
library."

ORIGIN

Alignment Scores:

Pred. No.:	9,096-59	Length:	811
Score:	509.00	Matches:	97
Percent Similarity:	98.98%	Conservative:	0
Best Local Similarity:	98.98%	Mismatches:	1
Query Match:	98.45%	Indels:	0
DB:	4	Gaps:	0

US-10-001-254-6 (1-98) x BE616438 (1-811)

Qy 1 ThTyrValArgCysLeuAenValGlyLeuIleArgLysLeuSerAappPheIleAspPro 20
Db 77 ACATATGCGCGCTCCCTCAATGTGACTAATTAAGAGCTGTCAGATTATTAATGATCCT 136
Qy 21 GlnGluGlyTrpLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
Db 137 CAAGAAGATGAGAGAAATTAGCTGTAGCTATTAACCATCTCGATGATGATGATAC 196
Qy 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
Db 197 AATCAGTTTCACATAGAGAGATTGAAGCATTACTTCAACGCGAAAGATCCCACTTCT 256
Qy 61 GluLeuLeuPheAspTTPGlyThrThrasnCythrValGlyAspLeuValAspLeu 80
Db 257 GAATTACTGTTGACTGGGGCCACCAATATGACAGATTGGATCTTGATCTTTTG 316
Qy 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
Db 317 ATCAAATAGATTTCCTCTCCGCGAGCTTTTGTCCCAAGATGCTTCCC 370

RESULT 4 BE482619 402 bp mRNA linear EST 27-MAR-2003
LOCUS BE482619 168463 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE482619 GI:9602152
VERSION BE482619.1 GI:9602152
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE 1. (bases 1 to 402)
AUTHORS Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
and Quackenbush,J.
Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)

TITLE Contact: Sonstegard TS
JOURNAL USA, ARS, Beltsville Agricultural Research Center
MEDLINE Bldg. 200 Km 2A, Beltsville, MD 20705, USA
PUBMED Tel: 301 504 8416
12140684 Fax: 301 504 8414
COMMENT Email: tads@ipsl.barc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACAGC
Plate: 11 row: F column: 7
Seq primer: ATTATGCTGACACTATG.
Location/Qualifiers

FEATURES

SOURCE

1. 402
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="BARC 5BOV"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

ORIGIN

Alignment Scores:

Pred. No.:	2,896-57	Length:	402
Score:	495.00	Matches:	92
Percent Similarity:	97.96%	Conservative:	4
Best Local Similarity:	93.88%	Mismatches:	2
Query Match:	95.74%	Indels:	0
DB:	2	Gaps:	0

US-10-001-254-6 (1-98) x BE482619 (1-402)

Qy 1 ThTyrValArgCysLeuAenValGlyLeuIleArgLysLeuSerAappPheIleAspPro 20
Db 88 ACATATGCGCGCTCCCTCAATGTGACTAATTAAGAGCTGTCAGATTATTAATGATCCT 147
Qy 21 GlnGluGlyTrpLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
Db 148 CAAGAAGATGAGAGAAATTAGCTGTAGCTATTAACCATCTCGATGATGATGATAC 207
Qy 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
Db 208 AATCAGTTTCACATAGAGAGATTGAAGCATTACTGCAATATGAAAGCCCACTGCT 267
Qy 61 GluLeuLeuPheAspTTPGlyThrThrasnCythrValGlyAspLeuValAspLeu 80
Db 268 GAGTTACTGTTGACTGGGGCCACCAATATGACAGATTGGATCTTGATGATATTTTG 327
Qy 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
Db 328 GTCAAATAGATTTCCTCTCCGCGAGCTTTTGTCTACAGATGCTTACC 381

RESULT 5 CN788062 666 bp mRNA linear EST 26-MAY-2004
LOCUS CN788062 4122347 BARC 8BOV Bos taurus cDNA clone 8BOV_26007 5', mRNA
ACCESSION CN788062 GI:47684042
VERSION CN788062.1 GI:47684042
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE 1. (bases 1 to 666)
AUTHORS Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassel,C.P. and
Matukumalli,L.K.
Construction and Analysis of a cDNA Library Generated From
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
Unpublished (2004)
Contact: Richard G. Baumann
Bovine Functional Genomics Lab

TITLE Contact: Sonstegard TS
JOURNAL USA, ARS, Beltsville Agricultural Research Center
MEDLINE Bldg. 200 Km 2A, Beltsville, MD 20705, USA
PUBMED Tel: 301 504 8416
12140684 Fax: 301 504 8414
COMMENT Email: tads@ipsl.barc.usda.gov

ANRI
BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744
Email: rbaumann@anri.barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt '- -trim_fast. Vector identified
by cross_match using options -mismatch 12 -minscore 18
Plate: 26 row: 0 column: 07
Seq primer: CCTATTAGTGCACCTATAGAC
High quality sequence stop: 666.

FEATURES

source

Location/Qualifiers
1..666
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="8BOV 26007"
/sex="Female"
/tissue_type="Epithelial, Muscle"
/dev_stage="Lactating, Neonatal"
/lab_host="DH10B Tona"
/clone_1ib="BARC 8BOV"
/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site_1:
Not; Site_2: EcoRI; Normalized cow cDNA intestinal
library in pCMVSPORT6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 lactating, proximal duodenum,
jejunum, distal ileum, colon, 1/5 Neonatal, proximal
duodenum, jejunum, distal ileum"

ORIGIN

Alignment Scores:

Pred. No.: 5.74e-57 Length: 666
Score: 495.00 Matches: 92
Percent Similarity: 97.96% Conservative: 4
Best Local Similarity: 93.88% Mismatches: 2
Query Match: 95.74% Indels: 0
DB: 7 Gaps: 0

US-10-001-254-6 (1-98) x CN788062 (1-666)

QY 1 ThrTyrValArgCysLeuAenValGlyLeuIleArgIysLeuSerAspPheIleApro 20
DB 69 ACATACGTGGCGCTCCCTCACTTGAATTAAGAGTGTCCGATTTTATGATCCT 128
QY 21 GlnGluGlyTTrpIlyslsleuAvalAlaIleIlyslsProSerGlyAspAspArgTyr 40
DB 129 CAAAGAGATGAGAGAGATTAGCAGTCGTATTAACCAATCTGTGATGATATAC 188
QY 41 AengInPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyIysSerProThrSer 60
DB 189 AATCAGTTTCACATTAAGAGATTGAGCACTTACTCAATGGAAGAAAGCCCACTGT 248
QY 61 GluLeuLeuPheAspTrpIlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
DB 249 GAGTACTGTTTGGACGGGGCACCAAAATTGACAGTTGGATCTTGTGATATTTTG 308
QY 81 IlegInaEngIuPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
DB 309 GTCCAAAATGATTTTGTCCCTGCAAGTCTTTTGTCTACAGATGCTGTACCC 362

RESULT 6
LOCUS Bf696981 719 bp mRNA linear EST 22-DEC-2000
DEFINITION 602130160P1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287014 5',
mRNA sequence.
ACCESSION Bf696981
VERSION Bf696981.1 GI:11982389
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
1 (bases 1 to 719)
AUTHORS NIH-MGC
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: LLCMH124 row: 9 column: 15
High quality sequence stop: 632.

FEATURES

source

Location/Qualifiers
1..719
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4287014"
/tissue_type="Primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1ib="NIH MGC 56"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgccgcgcgc); Site_2: SfiI (ggccattatggc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGCGC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCCGCGCGCCGACATG-AT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

ORIGIN

Alignment Scores:

Pred. No.: 1.49e-55 Length: 719
Score: 485.00 Matches: 97
Percent Similarity: 97.00% Conservative: 0
Best Local Similarity: 97.00% Mismatches: 1
Query Match: 93.81% Indels: 2
DB: 2 Gaps: 0

US-10-001-254-6 (1-98) x Bf696981 (1-719)

QY 1 ThrTyrValArgCysLeuAenValGlyLeuIleArgIysLeuSerAspPheIleApro 20
DB 92 ACATATGCGCCTCCCTCAATGTTGAGCTAATTAGGAAGCTGCAGATTTTATGATCCT 151
QY 21 GlnGluGlyTTrpIlyslsleuAvalAlaIleIlyslsProSerGlyAspAspArgTyr 40
DB 152 CAAAGAGATGAGAGAGATTAGCAGTCGTATTAACCAATCTGTGATGATATAC 211
QY 41 AengInPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyIysSerProThrSer 60
DB 212 AATCAGTTTCACATTAAGAGATTGAGCACTTACTCAATGGAAGAAAGCCCACTGT 271
QY 61 GluLeuLeuPheAspTrpIlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
DB 272 GAATTACTGTTTGGACGGGGCACCAAAATTGACAGTTGGATCTTGTGATATTTTG 331
QY 80 uIlegInaEngIuPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
DB 332 GATCCAAATGATTTTGTGCTCTGCAAGTCTTTTGTCTCCCAAGTGTGTTCC 387

RESULT 7
LOCUS CA538859 503 bp mRNA linear EST 19-NOV-2002
DEFINITION C0272B01-5N NIA Mouse 7.5-dpc Embryo cDNA library (Long) Mus
musculus cDNA clone NIA:C0272B01 IMAGE:30017484 5', mRNA sequence.

ACCESSION CA538659
 VERSION CA538659.1 GI:25080828
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 AUTHORS 1 (bases 1 to 503)
 Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Tanaka, T., Lim, M.K.,
 Luo, A. and Ko, M.S.H.
 TITLE Systematic Analyses of NIA Mouse 7.5-dpc Whole Embryo cDNA Library
 (Long)
 JOURNAL Unpublished (2001)
 COMMENT Other ESTs: C0272B01-3
 Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.igs.nia.nih.gov
 Plate: C0272 row: B column: 01
 Seq primer: M13 Reverse
 High quality sequence stop: 503
 POLYA=No.

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FEATURES
Source

Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="nlaEST:C0272B01-5N"
/db_xref="taxon:10090"
/clone="NIA:C0272B01 IMAGE:30017484"
/tissue_type="whole embryo including extraembryonic
tissues at 7.5-days postcoitum"
/dev_stage="7.5-days postcoitum"
/lab_host="DH10B"
/clone_idb="NIA Mouse 7.5-dpc Whole Embryo cDNA Library
(Long)"
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
extracted from a pool of four embryos at 7.5-days
postcoitum. Double-stranded cDNAs were synthesized with an
Oligo(dT) primer [Invitrogen:
5'-GACACTGCTCAGATCGGACGCGCCGCTTTTTTTTTTTT-3'] from
7 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lone-linker L1-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.2 kb. The library was constructed
by Yulan Piao (NIA)."

```

ORIGIN	
Alignment Scores:	
Pred. No.:	1.56e-54
Score:	476.00
Percent Similarity:	95.92%
Best Local Similarity:	90.82%
Query Match:	92.07%
DB:	6
	Gaps: 0
US-10-001-254-6 (1-98) x CA538859 (1-503)	
QY	1 ThrYrYValArgCYbLueuAsnValGlyLeuIleArgLYsLeuSerApPheIleApPro 20

Accession	Protein	Length
Db	ACATCAATCAACCAACCTTAATGTGGGAGATCCCTTAGAAGCTGTCCGATTATTATGATCCCT	251
Qy	GIINGUGLYTPPLVSLVLEUALAVAIALAEVLVSPVPSERGLVASPAPAGLYR	40
Db	CAAGAGGCTGGAGAAATTAGCACTACTACAAAGCCCTCCGCGACACAGATAC	311
Qy	AEINGINPHEHSLIETGIRPHEGLUALAEULEUGINTHGLYLSERPROTHSER	60
Db	AATCAGTTCCATATNAGAGAGATCCAGACCTTACTTCAGACCCGGAGAGGCCCACTGT	371
Qy	GLUTEULEUPHEASPTIRPGLYTHRTHIRASCYSTRIVALGLYASPLEUVALASPLEULEU	80
Db	GAAGCTGCTGTGAACTGGGGGACCCAGAACTCAGAGTTGGGCACTTGTGATCTACTG	431
Qy	ILLEGINANGUPHEPHEALAPROLAJASERLEULEULEUPROASPLALAVAIPro	98
Db	GTCCAGATGAGCTGTTGGCCCCCGCCACTCTCTCTGCTCCGGATGCCCTTCCC	485

RESULT	8
B0552228	
LOCUS	
DEFINITION	B0552228 598 bp mRNA linear EST 20-JUN-2002
LOCUS	H4014609-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
DEFINITION	H4014609 5' mRNA sequence.
LOCUS	B0552228
DEFINITION	B0552228.1 GI:21453114
LOCUS	Est.
DEFINITION	Mus musculus (house mouse)

ORGANISM	REFERENCE	AUTHORS
<i>Mus musculus</i>		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Rodentia; Scuriurognathi; Muridae; Murinae; Mus.		
1 (bases 1 to 586)		
Vanburen, V., Piao, Y., Dudekula, D. B., Qian, Y., Carter, M. G.,		

TITLE	Matlin, P. R., Stagy, C. A., Bassey, U., Alta, K., Hamtani, T., Katagiri, G. J., Luo, A. G., Kelsio, J., Hide, W., and Ko, M. S. H. Assembly, verification, and initial annotation of NIA 7.4k mouse cDNA clone set
JOURNAL	Genome Res. 12 (12), 1999-2003 (2002)
MEDLINE	22354164
PUBMED	12466305
COMMENT	Contact: Yong Qian

COMMENT

Contact: Yong Qian
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA_NIA_7_4k.html for details.
Plate: H4014 row: C column: 09
Seq primer: -21M13 Reverse
High quality sequence stop: 598
POLYA=No.

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FEATURES
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location/Qualifiers
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    /db_xref="tlaEST:H4014C09-5"
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    /clone="H4014C09"
    /sex="mixed"
    /dev_stage="mixed"
    /lab_host="DH10B"
    /clone_lib="NIA Mouse 7.4K cDNA Clone Set"
    /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
clone is among a rearranged set of 7,407 clones from more
than 20 cDNA libraries."

```

ORIGIN	
Alignment Scores:	
Pred. No.:	1,98e-54
Score:	476.00
Percent Similarity:	95.92%
Best Local Similarity:	90.82%
length:	598
Matches:	89
Conservative:	5
Mismatches:	4

clone_lib="RIKEN full-length enriched, 10 day neonate skin"
/note=Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'-GAGGAGAGAGAGATCCAAAGGCTCTTTTCTTTTCTTTTAA 3'], cDNA was prepared by using reversease thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of

Accession	Gene	Length (bp)	RNA	EST
BT721552	RIKEN full-length enriched, adult male diencephalon Mus musculus cDNA clone 9330209D03 5', mRNA sequence.	638	musculus	EST 17-DEC-2002
BT721552				
BT721552				
BT721552				
BT721552.1	GI:27134669			
EST.				
Mus musculus (house mouse)				
Mus musculus				
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
1 (bases 1 to 638)				
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaado, I., Otsu, N., Sato, R., Suzuki, H., Yamana, A., Kikawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gotohori, T., Baldirelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kampin, A., Maseda, H., Batolova, S., Beisel, K. W., Blake, J. A., Brad, D., Drusic, V., Chochia, C., Corbani, L. E., Cousins, S., Dalla, E., Dugan, T. A., Fletcher, C. P., Forrest, A., Frazer, K. S., Gaasterland, J., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawachi, H., Kawasawa, Y., Kedzierzki, R. M., King, B. L., Konagaya, A., Kurouchi, I. V., Lee, Y., Lennard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Perte, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravaei, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sanderlin, A., Schneider, C., Sempke, C. A., Setou, M., Shimada, K., Sultana, R., Takemura, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wymslaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakakuma, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Sakakuma, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,				

JOURNAL
MEDLINE
PUBMED
COMMENT

of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
12466851

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carrinci, P.,
Fukuda, S., Hashizume, M., Hayashida, K., Hirozane, T., Hori, F.,
Imetani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numazaki, R., Ohno, M., Ohse, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

FEATURES

SOURCE

Location/Qualifiers
1. 663
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="B230034103"
/sex="male"
/tissue_type="corpora quadrigemina"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male corpora
quadrigemina"
/note="Site 1: SalI, Site 2: BamHI, cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCTCAAGACTCTTTTCTTTTCTTTN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATCTCAAGATTAATTAATTAATCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I."

ORIGIN

Alignment Scores:
Pred. No.:
Score:
Percent Similarity:

2.28e-54 Length: 663
476.00 Matches: 89
95.92% Conservative: 5

Best Local Similarity: 90.82% Mismatches: 4
Query Match: 92.07% Indels: 0
DB: 6 Gaps: 0

US-10-001-254-6 (1-98) x BY726858 (1-663)

QY 1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgIysLeuSerAspPheIleAspPro 20
DB 185 ACATCATACCAACCAACTTAATGTGGGATCCTTGAAGAGCTGTGGATTTATGATCTCT 244
QY 21 GINGUGIYTPYLYSLYSLEALALALALEYSLYSPROSERGIYAASPARGYR 40
DB 245 CAAGAGGGTGGAGAAATTTGACGTGCTTCACAAAACCGTCCGGCAGACAGATAC 304
QY 41 AaanglnPheHisIleArgArgPheGluAlaLeuLeuGlnTrnGlyLysSerProThrSer 60
DB 305 AATCATGTTCCATTAAGAGATTTGAAACCTTACTTCAACCGGAGAGACCCCACTGT 364
QY 61 GluLeuLeuPheAspTIPGlyThrThrAsnGlyThrValGlyAspLeuValAspLeuLeu 80
DB 365 GAACGTGCTTTGACTGGGACACCAACAGTGCAGACCTTGATCTACTG 424
QY 81 IleglnAsngIuphePheAlaProAlaSerLeuLeuPProAspAlaValPro 98
DB 425 GTCCAGATTGAGCTGTTGGCCCCGCGCACTCTCTGTCGCGAGTCCGTTCCC 478

RESULT 13

LOCUS BB613167 676 bp mRNA linear EST 26-OCT-2001
DEFINITION BB613167 RIKEN full-length enriched, 10 day neonate skin Mus
ACCESSION BB613167
VERSION BB613167.1 GI:16453871
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 676)
AUTHORS Arikawa, T., Carrinci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, D.,
Konno, H., Konda, M., Koya, S., Matsumura, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arikawa, T., et al. 2001)
Unpublished (2001)

TITLE

JOURNAL
COMMENT
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Carrinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iwata, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Kira, A.,
Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, K.,
and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carrinci, P.,
Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: January 12, 2005, 06:32:57 ; Search time 88 Seconds
(without alignments)
791.560 Million cell updates/sec

Title: US-10-001-254-6
Sequence: 1 TYVRCINLVGIRKLSDFIDP.....LLIGNEPFAPASLLPDAVP 98

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Xgapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

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Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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5: /cgn2_6/ptodata/1/ina/PCtUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	517	100.0	833	4	US-09-166-350-10
2	517	100.0	2817	4	US-09-966-451-3
3	236	49.5	31000	4	US-09-966-451-10
4	96.5	18.7	2288	3	US-09-135-232-1
5	96.5	18.7	2288	4	US-09-863-549-1
6	79	15.3	1806	2	US-08-980-060-1
7	79	15.3	1806	2	US-09-307-185-1
8	79	15.3	1806	4	US-09-773-753-1
9	79	15.3	3459	2	US-08-980-060-3
10	79	15.3	3459	3	US-09-307-185-3
11	79	15.3	3459	4	US-09-773-753-3
12	78.5	15.2	479	2	US-08-980-060-14

C 13	78.5	15.2	479	3	US-09-307-185-14	Sequence 14, Appl
C 14	78.5	15.2	479	4	US-09-773-753-14	Sequence 14, Appl
C 15	72	13.9	536165	4	US-09-214-808-1	Sequence 1, Appl
C 16	70.5	13.6	901	4	US-09-799-451-434	Sequence 43, App
17	69.5	13.4	1416	3	US-09-234-393-26	Sequence 26, Appl
18	69.5	13.4	1416	4	US-09-360-545-19	Sequence 19, Appl
19	69.5	13.4	1416	4	US-09-865-171-26	Sequence 26, Appl
20	69.5	13.4	1785	3	US-09-234-393-49	Sequence 49, Appl
21	69.5	13.4	1785	3	US-09-234-393-51	Sequence 51, Appl
22	69.5	13.4	1785	3	US-09-234-393-53	Sequence 53, Appl
23	69.5	13.4	1785	4	US-09-865-171-49	Sequence 49, Appl
24	69.5	13.4	1785	4	US-09-865-171-51	Sequence 51, Appl
25	69.5	13.4	1785	4	US-09-865-171-53	Sequence 53, Appl
26	69.5	13.4	1785	4	US-09-398-393-49	Sequence 49, Appl
27	69.5	13.4	1785	4	US-09-887-586A-49	Sequence 49, Appl
28	69.5	13.4	1785	4	US-09-895-752-49	Sequence 49, Appl
29	69.5	13.4	1785	4	US-09-903-012B-49	Sequence 49, Appl
30	69.5	13.4	1785	4	US-09-900-797-49	Sequence 49, Appl
31	69.5	13.4	1977	3	US-09-234-393-23	Sequence 23, Appl
32	69.5	13.4	1977	4	US-09-865-171-23	Sequence 23, Appl
33	66.5	12.9	265	4	US-09-313-284A-3660	Sequence 3660, Ap
34	66.5	12.9	648	4	US-09-489-039A-5677	Sequence 5677, Ap
35	66	12.8	213	4	US-09-248-796A-7045	Sequence 7045, Ap
36	66	12.8	837	4	US-09-248-796A-2167	Sequence 2167, Ap
37	66	12.8	987	4	US-09-252-991A-11251	Sequence 11251, A
38	66	12.8	1140	4	US-09-252-991A-10937	Sequence 10937, A
C 39	66	12.8	3141	4	US-09-854-133-306	Sequence 306, App
C 40	65	12.6	1623	4	US-09-513-783A-33	Sequence 33, Appl
C 41	65	12.6	1623	4	US-09-430-656-33	Sequence 33, Appl
C 42	65	12.6	1623	3	US-09-134-001C-470	Sequence 470, App
C 43	64.5	12.5	1521	3	US-09-534-228B-6	Sequence 6, Appl
C 44	64.5	12.5	1521	4	US-09-710-279-4327	Sequence 4327, Ap
C 45	64.5	12.5	4066	4		

ALIGNMENTS

RESULT 1
US-09-166-350-10
; Sequence 10, Application US/09166350A
; Patent No. 6440663
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Chen, Yao
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Old, Lloyd
; APPLICANT: Jager, Elke
; TITLE OF INVENTION: Renal Cancer Associated Antigens and
; TITLE OF INVENTION: Uses Therefor
; FILE REFERENCE: L0461/7051
; CURRENT APPLICATION NUMBER: US/09/166,350A
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: US 09/166,350
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 833
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-166-350-10
Alignment Scores:
Pred. No.: 3.96e-72
Score: 517.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Gaps: 0
US-10-001-254-6 (1-98) x US-09-166-350-10 (1-833)

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QY 1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20
Db 74 ACNATATGCGCTCCCTCAATGTTGAGCTAATTAGAAAGCTGTGACGATTTATTAATGATCCT 133
QY 21 GlnGluGlyTTPylsLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
Db 134 CAAGAGAGATGAGAAAGAGTTAGCTGATGCTATTAATAAACCATCTGGTGATGATAGATAC 193
QY 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
Db 194 AATCAGTTTCACTAAGAGATTTGAGATTAAGCATTAATCAAACTGGAAGAAAGTCCACTTCT 253
QY 61 GluLeuLeuPheAspTTPGlyThrThrAsnCystrValGlyAspLeuValAspLeuLeu 80
Db 254 GAATTAAGTGTGAGCTGGGACCAAAATTTGACAGTTGGTGTATCTTTGGATCTTTTG 313
QY 81 IleGlnAsnGlnPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
Db 314 ATCCAAATGAATTTTGTCTCTCGAGCTTTTGTCTCCAGATGCTGTTCCC 367

RESULT 2
US-09-966-451-3
; Sequence 3, Application US/09966451
; Patent No. 6692959
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
; FILE REFERENCE: RTS-0324
; CURRENT APPLICATION NUMBER: US/09/966,451
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)...(1432)
US-09-966-451-3

Alignment Scores:
Pred. No.: 2,566-71 Length: 2817
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-001-254-6 (1-98) x US-09-966-451-3 (1-2817)
QY 1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20
Db 74 ACNATATGCGCTCCCTCAATGTTGAGCTAATTAGAAAGCTGTGACGATTTATTAATGATCCT 133
QY 21 GlnGluGlyTTPylsLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
Db 134 CAAGAGAGATGAGAAAGAGTTAGCTGATGCTATTAATAAACCATCTGGTGATGATAGATAC 193
QY 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
Db 194 AATCAGTTTCACTAAGAGATTTGAGATTAAGCATTAATCAAACTGGAAGAAAGTCCACTTCT 253
QY 61 GluLeuLeuPheAspTTPGlyThrThrAsnCystrValGlyAspLeuValAspLeuLeu 80
Db 254 GAATTAAGTGTGAGCTGGGACCAAAATTTGACAGTTGGTGTATCTTTGGATCTTTTG 313
QY 81 IleGlnAsnGlnPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
Db 314 ATCCAAATGAATTTTGTCTCTCGAGCTTTTGTCTCCAGATGCTGTTCCC 367

RESULT 3
US-09-966-451-10
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; Sequence 10, Application US/09966451
; Patent No. 6692959
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
; FILE REFERENCE: RTS-0324
; CURRENT APPLICATION NUMBER: US/09/966,451
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 10
; LENGTH: 31000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-966-451-10

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Best Local Similarity: 98.00% Mismatches: 0
Query Match: 49.52% Indels: 0
DB: Gaps: 0

US-10-001-254-6 (1-98) x US-09-966-451-10 (1-31000)
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QY 65 AspTTPGlyThrThrAsnCystrValGlyAspLeuValAspLeuLeuIleGlnAsnGln 84
Db 13023 GACTGGGGACCAACAAATTTGACAGTTGTGATCTTTGATTCACCAAAATGAA 13082
QY 85 PhePheAlaProAlaSerLeuLeuLeuPro 94
Db 13083 TTTTGTCTCTCGAGATCTTTGTCTCCCA 13112

RESULT 4
US-09-135-232-1
; Sequence 1, Application US/09135232
; Patent No. 6262228
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaodan
; TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods
; FILE REFERENCE: T98-019
; CURRENT APPLICATION NUMBER: US/09/135,232
; CURRENT FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2288
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(1851)
US-09-135-232-1

Alignment Scores:
Pred. No.: 0,000102 Length: 2288
Score: 96.50 Matches: 23
Percent Similarity: 47.95% Conservative: 12
Best Local Similarity: 31.51% Mismatches: 31
Query Match: 18.67% Indels: 7
DB: Gaps: 1

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QY 8 ValGlyLeuIleArgLysLeuSerAspPheIleAspProGlnGluGlyTTPylsLysLeu 27
Db 136 CTCGAGAGCTTGCCTGCTGTTCTGAGACGCTGCGACGCGCTGCGCTGCGCGCTG 195
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Qy      28 AlValAlaIleuLysvProserGIyaRPaRdArGtYVaEnGIInPheNIElaRdArg 47
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Db      196 GCAGAGAGACTTCAAGC-----ACGTGGCTGGAAATTCCTCAT 234
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Qy      48 PheGluaLeuLeuGIInThrGIlySerProThSergIUleuPheAapTrpGIly 67
       |||          ::|
Db      235 ATTGAATAAGTAATAGACCAGGTAATAAGTGAAACAAGAATTACTTTGGTCTGGGCA 294
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Qy      68 ThrThrAsnCyeThrValGIlyARleuValARleuLeu 80
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Db      295 CAGAAAAACAAGACCAATCGGTGACCTTTTACAGAGTCTTC 333
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RESULT 5
US-09-863-549-1
; Sequence 1, Application US/09863549
; Patent No. 6576444
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaoan
; TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods
; FILE REFERENCE: T98-019
; CURRENT APPLICATION NUMBER: US/09/863,549
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/135,232
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2288
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(1851)
US-09-863-549-1

Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:

US-10-001-254-6 (1-98) x US-09-863-549-1 (1-2288)

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Qy     28 AlValAlaIleuLysvProserGIyaRPaRdArGtYVaEnGIInPheNIElaRdArg 47
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Qy     48 PheGluaLeuLeuGIInThrGIlyLSerProThSergIUleuPheAapTrpGIly 67
       |||          ::|
Db    235 ATTGAATAAGTAATAGACCAGGTAATAAGTGAAACAAGAATTACTTTGGTCTGGGCA 294
                               :|
Qy     68 ThrThrAsnCyeThrValGIlyARleuValARleuLeu 80
       |||          ::|
Db    295 CAGAAAAACAAGACCAATCGGTGACCTTTTACAGAGTCTTC 333
                               :|

RESULT 6
US-08-980-060-1
; Sequence 1, Application US/08980060
; Patent No. 5965421
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: PENG, PING
; APPLICANT: MUZIO, MARTA
; APPLICANT: DIXIT, VISHVA M.
; TITLE OF INVENTION: HUMAN IRAK-2
; NUMBER OF SEQUENCES: 14

```

```
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
/ STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600  
/ CITY: WASHINGTON  
/ STATE: D.C.  
/ COUNTRY: USA  
/ ZIP: 20005-3934  
  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patentin Release #1.0, Version #1.30  
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/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/980,060  
/ FILING DATE: Herewith  
/ CLASSIFICATION: 435  
  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: STEFFE, ERIC K.  
/ REGISTRATION NUMBER: 36,688  
/ REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (202) 371-2600  
/ TELEFAX: (202) 371-2540  
/ INFORMATION FOR SEQ ID NO.: 1:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 1806 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: double  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: DNA (genomic)  
/ FEATURE:  
/ NAME/KEY: CDS  
/ LOCATION: 34..1803  
/ US-08-980-060-1
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Best Local Similarity:	31.88%	Mismatches:	19
Query Match:	15.28%	Indels:	16
DB:	2	Gaps:	2

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US-10-001-254-6 (1-98) x US-08-980-060-1 (1-1806)
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OY	45	Ileargatgphgehalaleuleuglnthr--glylvsrProThSerGluLeulen	63
Db	157	CTGCAGGAATCAACATCATCATTGAGCGGGGTGTGTAGCATCACGCCGGAGCTGCTG	216
OY	64	pheaapTpglytThrThAsncythrValglAapbleuValAspleuenuliEgliAnsn	83
Db	217	TGGTGctggagcattccgcacgccaccgtCCAGCAAAttgttgaccttccttgtcgccgcttg	276
OY	84	GluPhepHealAprAlaserleuLeueu-----	93
Db	277	GAGCTCTAACGGGCGTCGCCAGACTATnctGaactGAAAcTGGAAACCGGCTCTGTAAtCAGGTGT	336
OY	94	-----PrOspHalaval 97	
Db	337	CCCATTCCAGCCTTCCTGACTCTGTG 363	

RESULT 7
US-09-307-185-1
Sequence 1, Application US/09307185
Patent No. 6222019
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: PENG, PING
APPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/307,185
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/980,060
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1806 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 34..1803
; US-09-307-185-1

Alignment Scores:
Pred. No.: 0.0423 Length: 1806
Score: 79.00 Matches: 22
Percent Similarity: 49.28% Conservative: 12
Best Local Similarity: 31.88% Mismatches: 19
Query Match: 15.28% Indels: 16
Gaps: 2

US-10-001-254-6 (1-98) x US-09-307-185-1 (1-1806)
QY 45 IleaTgATgPheGluAlaLeuLeuGlnThr---GLYSeSerProthrsSerGluLeuLeu 63
Db 157 CTGCGGAAGATCAAGTCCATCGAGCGGCGGTGTGAGCATCAAGCGGAGCTGTG 216
QY 64 PheaSPITPGLYThrThraNCyThrValGlyAspLeuValAspLeuLeuIleGlnaen 83
Db 217 TGGTGTTGGGGCATGCGGAGCGCCACCGTCAGCAACTTGTGAACTCTGTCGCCGCTG 276
QY 84 GluPhePheAlaProAlaSerLeuLeu----- 93
Db 277 GAGCTTACCGGGCTGCCAGATCATCTGAAGTGAACCGGCTCTGTAATCAGGTGT 336
QY 94 -----ProAspAlaVal 97
Db 337 CCCATTCCAGCCTTCCCTGACTCTGTG 363

RESULT 8
US-09-773-753-1
; Sequence 1, Application US/09773753
; Patent No. 6653452
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; PENG, PING
; MUZIO, MARTA
; DIXIT, VISHVA M.
; TITLE OF INVENTION: HUMAN IRAK-2

```

```

; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/773,753
; FILING DATE: 02-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/980,060
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1806 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 34..1803
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
; US-09-773-753-1

Alignment Scores:
Pred. No.: 0.0423 Length: 1806
Score: 79.00 Matches: 22
Percent Similarity: 49.28% Conservative: 12
Best Local Similarity: 31.88% Mismatches: 19
Query Match: 15.28% Indels: 16
Gaps: 2

US-10-001-254-6 (1-98) x US-09-773-753-1 (1-1806)
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QY 84 GluPhePheAlaProAlaSerLeuLeu----- 93
Db 277 GAGCTTACCGGGCTGCCAGATCATCTGAAGTGAACCGGCTCTGTAATCAGGTGT 336
QY 94 -----ProAspAlaVal 97
Db 337 CCCATTCCAGCCTTCCCTGACTCTGTG 363

RESULT 9
US-08-980-060-3
; Sequence 3, Application US/08980060
; Patent No. 5965421
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; PENG, PING

```

APPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,060
FILING DATE: Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3459 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 34..1908
US-08-980-060-3
Alignment Scores:
Pred. No.: 0.115 Length: 3459
Score: 79.00 Matches: 22
Percent Similarity: 49.28% Conservative: 12
Best Local Similarity: 31.88% Mismatches: 19
Query Match: 15.28% Indels: 16
Gaps: 2
US-10-001-254-6 (1-98) x US-08-980-060-3 (1-3459)
Qy 45 ILEARGARGHEGUALALEULEUJNTHR---GLYLSERPROTHRSERGLULEULEU 63
Db 157 CTGGCGAAGATCAAGTCATGAGCGGGGTGACGATCACCGGAGACTCTG 216
Qy 64 PHEASPTIPGLYTHRTAANCYSTRVALGYASPLEUVALASPLEULEULEGLN 83
Db 217 TGGGTGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 276
Qy 84 GLUPHEPHEALAPROALASERLEULEU----- 93
Db 277 GAGCTTACCGGGGTGCGGACGATCTGTAAGTGAACCGGCTCTGAATCAGGTGT 336
Qy 94 -----ProaspAlaVal 97
Db 337 CCATTCACGCTTCCTGACTCTGTG 363
RESULT 10
US-09-307-185-3
Sequence 3, Application US/09307185
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: PENG, PING
APPLICANT: MUZIO, MARTA

APPLICANT: DIXIT, VISHVA M.
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/307,185
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/980,060
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3459 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 34..1908
US-09-307-185-3
Alignment Scores:
Pred. No.: 0.115 Length: 3459
Score: 79.00 Matches: 22
Percent Similarity: 49.28% Conservative: 12
Best Local Similarity: 31.88% Mismatches: 19
Query Match: 15.28% Indels: 16
Gaps: 2
US-10-001-254-6 (1-98) x US-09-307-185-3 (1-3459)
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Db 157 CTGGCGAAGATCAAGTCATGAGCGGGGTGACGATCACCGGAGACTCTG 216
Qy 64 PHEASPTIPGLYTHRTAANCYSTRVALGYASPLEUVALASPLEULEULEGLN 83
Db 217 TGGGTGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 276
Qy 84 GLUPHEPHEALAPROALASERLEULEU----- 93
Db 277 GAGCTTACCGGGGTGCGGACGATCTGTAAGTGAACCGGCTCTGAATCAGGTGT 336
Qy 94 -----ProaspAlaVal 97
Db 337 CCATTCACGCTTCCTGACTCTGTG 363
RESULT 11
US-09-773-753-3
Sequence 3, Application US/09773753
GENERAL INFORMATION:
APPLICANT: NI, JIAN

```

FENG, PING
MUZIO, MARTA
DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/773,753
FILING DATE: 02-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/980,060
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AMK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3459 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 34..1908
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-773-753-3
Alignment Scores:
Pred. No.: 0.115 Length: 3459
Score: 79.00 Matches: 22
Percent Similarity: 49.28% Conservative: 12
Best Local Similarity: 31.88% Mismatches: 19
Query Match: 15.28% Indels: 16
Gaps: 2
DB: 4
US-10-001-254-6 (1-98) x US-09-773-753-3 (1-3459)
QY 45 IleaTgATgPheGluAlaLeuLeuGlnThr---GlyLysSerProThrSerGluLeuLeu 63
Db 157 CTGCGGAAGATCAAGTCATGAGCGGCGGTGACGATCTCACGGGAGAGCTGCTG 216
QY 64 PheaSpTPGlyThrThraSnCyThrValGlyAspLeuValAspLeuLeuIleGlnAen 83
Db 217 TGTGTGTGGGGCATGCGGAGCGCACCGTCCAGCAACTTGTGAGACTCTGTGCGGCTG 276
QY 84 GluPhePheAlaProAlaSerLeuLeu----- 93
Db 277 GAGCTCTACCGGGCTGCCAGATCTCTCGAAGCTGGAAACCGGCTCTGTAATCAGGTGT 336
QY 94 -----ProAspAlaVal 97
Db 337 CCCATTCCAGCCTTCCCTGACTCTGTG 363
RESULT 12
US-08-980-060-14/c
Sequence 14, Application US/08980060
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Patent No. 5965421
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: FENG, PING
APPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,060
FILING DATE: Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AMK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-980-060-14
Alignment Scores:
Pred. No.: 0.00664 Length: 479
Score: 78.50 Matches: 19
Percent Similarity: 60.00% Conservative: 11
Best Local Similarity: 38.00% Mismatches: 19
Query Match: 15.18% Indels: 1
Gaps: 1
DB: 2
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QY 45 IleaTgATgPheGluAlaLeuLeuGlnThr---GlyLysSerProThrSerGluLeuLeu 63
Db 244 CTGCGGAAGATCAAGTCATGAGCGGCGGTGACGATCTCACGGGAGAGCTGCTG 185
QY 64 PheaSpTPGlyThrThraSnCyThrValGlyAspLeuValAspLeuLeuIleGlnAen 83
Db 184 TGTGTGTGGGGCATGCGGAGCGCACCGTCCAGCAACTTGTGAGACTCTGTGCGGCTG 125
QY 84 GluPhePheAlaProAlaSerLeuLeu----- 93
Db 124 GAGCTCTACCGGGCTGCCAGATCTCTGTG 95
RESULT 13
US-09-307-185-14/c
Sequence 14, Application US/09307185
Patent No. 6222019
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: FENG, PING
APPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
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Page 7

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COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/773,753
FILING DATE: 02-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/980,060
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: cDNA
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-773-753-14

Alignment Scores:
Pred. Score: 0.00664 Length: 479
Score: 78.50 Matches: 19
Percent Similarity: 60.004 Conservative: 11
Best Local Similarity: 38.004 Mismatch: 19
Query Match: 15.188 Indels: 1
DB: 4 Gaps: 1
US-10-001-254-6 (1-98) x US-09-773-753-14 (1-479)

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Db 244 CTGGCGGAAATCATAGTCATGAGCGGGGTGACGGGTGTGATCATCAGCGGAGCTGCTG 185
Qy 64 PheAspTrrGlgYThrThraMcySthrValGlyAspleuValAAspleuLeuIleGlnAsn 83
Db 184 TGTGTGTGGGGGCAATGGCGGAGCCACCGATCCAGCAACTTGTGGACCTCTGTGCCGCTG 125
Qy 84 GluPhePheAlaProAlaSerLeuLeuLeu 93
Db 124 GAGCTTACGGGGCTGCCAGATCATCTGTG 95

RESULT 15
US-09-214-808-1
: Sequence 1, Application US/09214808A
: Patent No. 6475793
: GENERAL INFORMATION:
: APPLICANT: Rosenthal, Andre
: APPLICANT: Freiberg, Christoph
: APPLICANT: Perret, Xavier Philippe
: APPLICANT: Broughton, William John
: TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
: Patent No. 6475793
: TITLE OF INVENTION: Plasmid
: FILE REFERENCE: CARP0068
: CURRENT APPLICATION NUMBER: US/09/214,808A
: CURRENT FILING DATE: 1999-06-22
: PRIOR APPLICATION NUMBER: PCT/IB97/00950
: PRIOR FILING DATE: 1997-07-10
: NUMBER OF SEQ ID NOS: 1
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1

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LENGTH: 536165
TYPE: DNA
ORGANISM: Rhizobium
US-09-214-808-1

Alignment Scores:

Pred. No.:	3.37e+03	Length:	536165
Score:	72.00	Matches:	28
Percent Similarity:	47.06%	Conservative:	12
Best Local Similarity:	32.94%	Mismatches:	39
Query Match:	13.93%	Indels:	6
DB:	4	Gaps:	5

US-10-001-254-6 (1-98) x US-09-214-808-1 (1-536165)

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           |||||.....|.....|.....|.....|.....|.....|.....|.....|
QY      36  ---GlyAspAspArg--TyrAsnGlnPheHisIleArgArgPheGluAlaLeuLeuGln 53
           |||||.....|.....|.....|.....|.....|.....|.....|.....|
DB      97299  ACCGGCGATGACATCTGACTTGGCTCCCTGCAGATCCACCAATATCAATCTTGTTAG 97358
           |||||.....|.....|.....|.....|.....|.....|.....|.....|
QY      54  ThrGlyLysSerProthrSerGluLeuLeuPheAspTyrGlyThrThrAsnGlyThrVal 73
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DB      97416  TGAAGTGACTTACAGGCCGCGCTTCCAAATCCGCTTCTTATCCGCTCTTCAAAATTTG 97475
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QY      93  LeuProAspAlaVal 97
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DB      97476  GTGCAATCAATTTGT 97490
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Search completed: January 12, 2005, 08:54:30
Job time : 157 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 12, 2005, 05:41:00 ; Search time 3301 Seconds

(without alignments)
1403.935 Million cell updates/sec

Title: US-10-001-254-6

Perfect score: 517
Sequence: 1 TYVRCINVGILRLSDPFDP.....LLIONEPFAPASLLPDAVP 98

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPRO.spool/h/US10001254/runac_10012005.172738.10459/app.query.fasta_1.263
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb_hcg:*
3: gb_in:*
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5: gb_ov:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_ets:*
12: gb_by:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	517	100.0	1383	6	AX431306 Sequence
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5	517	100.0	1636	9	AY340962	AY340962 Homo sapi
6	517	100.0	1684	9	AY340963	AY340963 Homo sapi
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9	517	100.0	2817	6	AX431318	AX431318 Sequence
10	517	100.0	2817	6	AF155118	AF155118 Homo sapi
11	517	100.0	2820	9	AK000528	AK000528 Homo sapi
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14	513	99.2	1383	9	AF445802	AF445802 Homo sapi
15	513	99.2	1383	9	AY283670	AY283670 Homo sapi
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17	478	92.5	1751	9	AY340967	AY340967 Homo sapi
18	476	92.1	1542	6	AX196262	AX196262 Sequence
19	476	92.1	1542	10	AF445803	AF445803 Mus muscu
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21	413	79.9	501	6	AX321132	AX321132 Sequence
22	287	55.5	1452	5	AY616584	AY616584 Danto rer
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25	256	49.5	33033	9	AY186092	AY186092 Homo sapi
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37	230	44.5	205374	10	AC147160	AC147160 Mus muscu
38	123	23.8	786	11	BV075713	BV075713 S212P6044
39	121.5	23.5	2069	3	AK116443	AK116443 Ciona int
40	98.5	19.1	1730	10	MMU440757	MMU440757 Mus muscu
41	96.5	18.7	1791	6	AX056430	AX056430 Sequence
42	96.5	18.7	1891	9	BC069388	BC069388 Homo sapi
43	96.5	18.7	2277	6	AX057324	AX057324 Sequence
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ALIGNMENTS

RESULT 1
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DEFINITION Sequence 5 from Patent WO0240680.
ACCESSION AX431296
VERSION AX431296.1 GI:21656165
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Pawlowski, K., Fiorentino, L., Godzik, A., Lee, S. H., Reed, J. C.,
Roch, W. and Stenier-Liawen, F.
TITLE Novel death domain proteins
JOURNAL Patent: WO 0240680-A 5 23-MAY-2002;
BURNHAM INST (US)
FEATURES
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Alignment Scores:

Pred. No.: 1.4e-61 Length: 294
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-001-254-6 (1-98) x AX431296 (1-294)

QY 1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgIysLeuSerAspPheIleAspPro 20
DB 1 ACATATGTCGCGCTCCCAATGTTGACTAATTAGGAAGCTGTCAGATTTTATGATCT 60
QY 21 GlnGlnGlyTTPblyslsleuAlaValAlaIlelyslsProSerGlyAspAspArgTyr 40
DB 61 CAAGAAGATGAGAGAGATTAGCTGTAGCTATTAAAAACCATCTGGTGTATGATAGATAC 120
QY 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyIysSerProThrSer 60
DB 121 AATCAGTTTCACTAAGAGATTGTAAGCATTTACTTCAAACTGAAAAAGTCCCATCTT 180
QY 61 GlnLeuLeuPheAspTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
DB 181 GAATTAAGTCTTTGACTGGGACACCAAAATGACAGATGTTGATCTTTGGATCTTTTG 240
QY 81 IleGlnAsnGlnPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
DB 241 ATCAAAATGAATTTTGTCTCTCGAGTCTTTTGTCTCCCAATGCTGTTCCC 294

RESULT 2
LOCUS AR223870 833 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 10 from patent US 6440663.
ACCESSION AR223870
VERSION AR223870.1 GI:23332452
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 833)
AUTHORS Scanlan,M.J., Stockert,E., Chen,Y.-T., Old,L.J., Jager,E. and Knuth,A.
TITLE Renal cancer associated antigens and uses therefor
JOURNAL Patent: US 6440663-A 10 27-AUG-2002;
FEATURES
LOCATION/Qualifiers
source 1..833
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 4.94e-61 Length: 833
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-001-254-6 (1-98) x AR223870 (1-833)

QY 1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgIysLeuSerAspPheIleAspPro 20
DB 74 ACATATGTCGCGCTCCCAATGTTGACTAATTAGGAAGCTGTCAGATTTTATGATCT 133
QY 21 GlnGlnGlyTTPblyslsleuAlaValAlaIlelyslsProSerGlyAspAspArgTyr 40
DB 134 CAAGAAGATGAGAGAGATTAGCTGTAGCTATTAAAAACCATCTGGTGTATGATAGATAC 193
QY 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyIysSerProThrSer 60

DB 194 AATCAGTTTCACTAAGAGATTGTAAGCATTTACTTCAAACTGAAAAAGTCCCATCTCT 253

QY 61 GlnLeuLeuPheAspTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
DB 254 GAATTAAGTCTTTGACTGGGACACCAAAATGACAGATGTTGATCTTTGGATCTTTTG 313

QY 81 IleGlnAsnGlnPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
DB 314 ATCAAAATGAATTTTGTCTCTCGAGTCTTTTGTCTCCCAATGCTGTTCCC 367

RESULT 3

AX431306 1383 bp DNA linear PAT 28-JUN-2002
LOCUS Sequence 15 from Patent WO0240680.
DEFINITION AX431306
ACCESSION AX431306
VERSION AX431306.1 GI:21656175
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Pawlowski,K., Fiorentino,L., Godzik,A., Lee,S.H., Reed,J.C., Roth,W. and Stenner-Liewen,F.
TITLE Novel death domain proteins
JOURNAL Patent: WO 0240680-A 15 23-MAY-2002;
BURNHAM INST (US)

FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

CDS

1..1383
/note="unnamed protein product"
/codon_start=1
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/db_xref="GI:21656176"
/translation="MNKPTIPSTVYRGLANGVLRKLSDFTPDQSGKKLAVAKRPSG
DDRYNPHIRREALLQIGKSPSTSEILFDMGTNCTVBDLVLLIQNEFPADASILLP
DAVRKNTATLPSKAITVQOKMPCKDKTLWTVPQNLQSYMPDSSPENKSLAV
SDTRPHSFSFELKNVNFDERPISVGKRMEGGGVVKKGVNNTVAAYKLAAM
VDITTEELKQDFDEIKVMAKCOHEINVELIGFSSDGDLCIVYVMPNGSLDRSLC
LDGTPPLSMHNRCKIAOGANGINFLHNIHRDIKSNVILDEAFATKISDFGAR
ASEKPAQVTMTSRIVGTTAAYAPALRGELTPKSDIYSRGVTLLFTIGLPAVDHRE
POLLDIKERHDEKTIIDYIDKKNNDSTSEAMTSVASQCLHEKKAKRPDIKV
QQLQENTAS"

ORIGIN

Alignment Scores:
Pred. No.: 9.14e-61 Length: 1383
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-001-254-6 (1-98) x AX431306 (1-1383)

QY 1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgIysLeuSerAspPheIleAspPro 20
DB 25 ACATATGTCGCGCTCCCAATGTTGACTAATTAGGAAGCTGTCAGATTTTATGATCT 84
QY 21 GlnGlnGlyTTPblyslsleuAlaValAlaIlelyslsProSerGlyAspAspArgTyr 40
DB 85 CAAGAAGATGAGAGAGATTAGCTGTAGCTATTAAAAACCATCTGGTGTATGATAGATAC 144
QY 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyIysSerProThrSer 60
DB 145 AATCAGTTTCACTAAGAGATTGTAAGCATTTCTCAAACTGAAAAAGTCCCATCTCT 204
QY 61 GlnLeuLeuPheAspTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80

Db	205	GAATTACTGTTTGA	CTGGGGCACCACCAAAATTCGACAGTTGGTGAATCTTGATCTTTTG	264
Qy	81	IIleGlnAsnGluPhePheAlaProAlaSerLeuLeuPProAlaValPro	98	
Db	265	ATCCAAATGAAATTTTTCCTGCTGCGAGCTTTTGTCTCCAGATGCTTCCC	318	
RESULT 4				
BC013316				
LOCUS	BC013316	1629 bp	mRNA	linear
DEFINITION	Homo sapiens interleukin-1 receptor-associated kinase 4, mRNA (CDNA			
ACCESSION	clone MGC:13330 IMAGE:4287014), complete cds.			
VERSION	BC013316			
KEYWORDS	BC013316.1 GI:15426431			
SOURCE	MGC.			
ORGANISM	Homo sapiens (human)			
REFERENCE	1	(bases 1 to 1629)		
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Kana, S.S., Loquai, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hu, Y.S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Butcherfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schnerker, A., Schein, J.E., Jones, S.J., and Marra, M.A.			
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99	(26)	16899-16903 (2002)
PUBMED	12477932			
REFERENCE	2	(bases 1 to 1629)		
AUTHORS	Strausberg, R.			
TITLE	Direct Submission			
JOURNAL	Submitted (31-AUG-2001)			
REMARK	Submitted (31-AUG-2001)			
COMMENT	Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA			
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov			
COMMENT	Contact: MGC help desk			
	Email: cgabbe-remail.nih.gov			
	Tissue Procurement: ATCC			
	cDNA Library Preparation: CLONTECH Laboratories, Inc.			
	DNA Sequencing by: The I.M.A.G.E. Consortium (LNU)			
	http://www.systemsbio.org			
	contact: amadan@systemsbiology.org			
	Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting			
FEATURES				
source	1. 1629			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/clone="MGC:13330 IMAGE:4287014"			
	/cise_type="Brain, primitive neuroectodermal"			
	/clone_id="NIH_MGC_56"			
gene				
CDS				
ORIGIN				
Alignment Scores:				
Pred. No.:	1,11e-60	Length:	1629	
Score:	517.00	Matches:	98	
Percent Similarity:	100.00%	Conservative:	0	
Best local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	9	Gaps:	0	
US-10-001-254-6 (1-98) x BC013316 (1-1629)				
Qy	1	ThrTyrValArgCysLeuAsnValGlyLeuIleArgGlySerSerAspPheIleAspPro	20	
Db	95	ACATATGTGGCGGCTCCATATGTTGACATATGGAAGCTGTCCAGATTTATGATCT	154	
Qy	21	GlnGluGlyTyrPheLeuAlaValAlaIleLeuLeuPProSerGlyAspAspArgTyr	40	
Db	155	CAAGAAAGATGGAAGAAAGTTAGCTGATTAATAAAACCACTGGTATGATAGATAC	214	
Qy	41	AsnGlnPheHilEileArgGlyPheGluAlaLeuLeuGlnThrGlyLeuSerProThrSer	60	
Db	215	AATCAGTTTCACATTAAGCAGATTGGAAGCATTTCTCAAACTGGAAAAAGCTCCACTTCT	274	
Qy	61	GluLeuLeuPheAspTyrPgiYThrThrAsnCysThrValGlyAspLeuValAspLeuLeu	80	
Db	275	GAATTACTGTTTGCCTGGGACACCAAAATTCGACAGTGTATCTTGGATCTTTTG	334	
Qy	81	IIleGlnAsnGluPhePheAlaProAlaSerLeuLeuPProAlaValPro	98	
Db	335	ATCCAAATGAAATTTTTCCTGCTGCGAGCTTTTGTCTCCAGATGCTTCCC	388	
RESULT 5				
AY340962				
LOCUS	AY340962	1636 bp	mRNA	linear
DEFINITION	Homo sapiens interleukin-1 receptor-associated kinase 4 (IRAK4)			
ACCESSION	AY340962			
VERSION	AY340962.1			
KEYWORDS	GI:37727958			
SOURCE	Homo sapiens (human)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
REFERENCE	1	(bases 1 to 1636)		
AUTHORS	Chuang, T.H., and Ulevitch, R.J.			
TITLE	Human interleukin-1 receptor associated kinase 4 cDNA sequences			
JOURNAL	Unpublished			
REFERENCE	2	(bases 1 to 1636)		

AUTHORS Chuang, T.H. and Ulevitch, R.J.
TITLE Direct Submission
JOURNAL Submitted (14-JUL-2003) Immunology, The Scripps Research Institute,
 10550 North Torrey Pines Rd., La Jolla, CA 92037, USA
FEATURES Location/Qualifiers

source
 1. 1636
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 /chromosome="12"
 /map="12q12"
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 1. 1636
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 65. 1448
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 /protein_id="AA02358.1"
 /db_xref="GI:37727959"
 /translation="MNKPIPTSTYVRCINVLIRKLSDFIDPQEGMKLAIVAKRPSG
 DRYNPFHRRPFAILLQTKSPTESELLFPMGTNTCTVGLVDLLIONEPFAPASLLP
 DAVPKTANTLPSEKALITVOOKMPFCDKRTMTPVONLEQSYMPDSSPENKSLV
 SDTRPHSFSEYELKNVTNNPDERPISVGNKMGEGGVYKGYVNTTVAYKLAAM
 VDTITPELKOQFDEIKVAKCOHENLVELGSSDGDCLIVYVMPGSLDLRLSC
 LDGTPPLSMWRCKIAQGANGLINFLHNHHRDIKSNAILDEAFKIDSGILAR
 ASEKPAQIVMTSRIVGTGTAYMAPEALRGITPESDIYSFGVULLEITGLPVDHRE
 POLLLDIKEIDEKTIIDYIDIKKNADSDTSVEAMYSVASQCLHEKKNKRPDIKV
 QQLQEMTAS"

ORIGIN

Alignment Scores:
 Pred. No.: 1.12e-60 Length: 1636
 Score: 517.00 Matches: 98
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-001-254-6 (1-98) x AY340962 (1-1636)

QY 1 ThrTrrValArgCysLeuAsnValGlyLeuIleArgLyLeuSerAspPheIleAspPro 20
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Db 90 ACAATATGGCGCTGCTCAATGTTGACATATTAGAACGCTGACATTTTATGATCCT 149
 |||||
QY 21 GlnGluGlyTrpLysLysLeuAlaValAlaIleLysProSerGlyAspAspArgTyr 40
 |||||
Db 150 CAAGAAGATGAGAAAGATTAGCTAGCTATTAAAAACCATCTGGTATGATGATAC 209
 |||||
QY 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
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Db 210 AATCAGTTTCACTATAGAGATTGAGCATTTCAACTGAAAGAAAGTCCCACTTCT 269
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QY 61 GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
 |||||
Db 270 GAATTAAGTCTTGGCTGGGACCAACAATTCACAGTTGGATCTTGATCTTTTG 329
 |||||
QY 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
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Db 330 ATCCAAATGAATTTTGTCTCTCGAGTCTTTTGTCTCCAGATGCTGTCTCC 383
 |||||

RESULT 6
 LOCUS AY340963 1684 bp mRNA linear PRI 01-AUG-2004
 DEFINITION Homo sapiens interleukin-1 receptor-associated kinase 4 variant
 (IRAK4) mRNA, complete cds; alternatively spliced.
 ACCESSION AY340963
 VERSION AY340963.1 GI:37727960
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 1 (bases 1 to 1684)
AUTHORS Chuang, T.H. and Ulevitch, R.J.
TITLE Human interleukin-1 receptor associated kinase 4 cDNA sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1684)
AUTHORS Chuang, T.H. and Ulevitch, R.J.
TITLE Direct Submission
JOURNAL Submitted (14-JUL-2003) Immunology, The Scripps Research Institute,
 10550 North Torrey Pines Rd., La Jolla, CA 92037, USA
FEATURES Location/Qualifiers

source
 1. 1684
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 /map="12q12"
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 1. 1684
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 114. 1496
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 /product="interleukin-1 receptor-associated kinase 4
 variant"
 /protein_id="AA02359.1"
 /db_xref="GI:37727961"
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 DRYNPFHRRPFAILLQTKSPTESELLFPMGTNTCTVGLVDLLIONEPFAPASLLP
 DAVPKTANTLPSEKALITVOOKMPFCDKRTMTPVONLEQSYMPDSSPENKSLV
 SDTRPHSFSEYELKNVTNNPDERPISVGNKMGEGGVYKGYVNTTVAYKLAAM
 VDTITPELKOQFDEIKVAKCOHENLVELGSSDGDCLIVYVMPGSLDLRLSC
 LDGTPPLSMWRCKIAQGANGLINFLHNHHRDIKSNAILDEAFKIDSGILAR
 ASEKPAQIVMTSRIVGTGTAYMAPEALRGITPESDIYSFGVULLEITGLPVDHRE
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 QQLQEMTAS"

ORIGIN

Alignment Scores:
 Pred. No.: 1.16e-60 Length: 1684
 Score: 517.00 Matches: 98
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-001-254-6 (1-98) x AY340963 (1-1684)

QY 1 ThrTrrValArgCysLeuAsnValGlyLeuIleArgLyLeuSerAspPheIleAspPro 20
 |||||
Db 138 ACAATATGGCGCTGCTCAATGTTGACATATTAGAACGCTGACATTTTATGATCCT 197
 |||||
QY 21 GlnGluGlyTrpLysLysLeuAlaValAlaIleLysProSerGlyAspAspArgTyr 40
 |||||
Db 198 CAAGAAGATGAGAAAGATTAGCTAGCTATTAAAAACCATCTGGTATGATGATAC 257
 |||||
QY 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
 |||||
Db 258 AATCAGTTTCACTATAGAGATTGAGCATTTCAACTGAAAGAAAGTCCCACTTCT 317
 |||||
QY 61 GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
 |||||
Db 318 GAATTAAGTCTTGGCTGGGACCAACAATTCACAGTTGGATCTTGATCTTTTG 377
 |||||
QY 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
 |||||
Db 378 ATCCAAATGAATTTTGTCTCTCGAGTCTTTTGTCTCCAGATGCTGTCTCC 431
 |||||

RESULT 7
 LOCUS CQ728380 2775 bp DNA linear PAT 03-FEB-2004
 DEFINITION Sequence 14314 from Patent WO02068579.

ACCESSION CQ728380
VERSION CQ728380.1 GI:42297030
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kites, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
Patent: WO 02068579-A 14314 06-SEP-2002;
PE Corporation (NY) (US)

FEATURES
source
1..2775
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN

Alignment Scores:
Pred. No.: 2,13e-60 Length: 2775
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-001-254-6 (1-98) x CQ728380 (1-2775)

Qy 1 ThrTyrValArgCysLeuAenValGlyLeuIleArgLysLeuSerAaspPheIleaspPro 20
Db 36 ACATATGCGCTGCCCTCAATGTGGACTAATVAGAAAGCTGCAGATTATTAATGATCCT 95

Qy 21 GlnGluGlyTTPylsYlsLeuAlaValAlaIleYlsYsProSergLYAaspAargTYr 40
Db 96 CAAGAAGATGGAAGAGATTAGCTGTAGCTATTAATAAACATCTGCGATGATAGATAC 155

Qy 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
Db 156 AATCAGTTTCACATAGAGAGATTGAGCATTAATCAAACTGGAAAAAGTCCACATCTCT 215

Qy 61 GluLeuLeuPheAspTPGlyThrThrAsnCysThrValGlyAaspLeuValAaspLeu 80
Db 216 GAATTACTGTTGACTGGGACCAACAATTGCACAGTTGATGATCTTGATCTTTTG 275

Qy 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAaspAlaValPro 98
Db 276 ATCCAAATGAATTTTTCCTCTGCGAGTCTTTTGTCCCGATGCTGTTCCC 329

RESULT 8
AR475548 2817 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 3 from patent US 6692959.
DEFINITION AR475548
ACCESSION AR475548
VERSION AR475548.1 GI:42715031
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2817)
AUTHORS Bennett, C.F. and Freier, S.M.
TITLE Antisense modulation of IL-1 receptor-associated kinase-4 expression
JOURNAL Patent: US 6692959-A 3 17-FEB-2004;
FEATURES
source
1..2817
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 2,17e-60 Length: 2817
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-001-254-6 (1-98) x AR475548 (1-2817)

Qy 1 ThrTyrValArgCysLeuAenValGlyLeuIleArgLysLeuSerAaspPheIleaspPro 20
Db 74 ACATATGCGCTGCCCTCAATGTGGACTAATVAGAAAGCTGCAGATTATTAATGATCCT 133

Qy 21 GlnGluGlyTTPylsYlsLeuAlaValAlaIleYlsYsProSergLYAaspAargTYr 40
Db 134 CAAGAAGATGGAAGAGATTAGCTGTAGCTATTAATAAACATCTGCGATGATAGATAC 193

Qy 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
Db 194 AATCAGTTTCACATAGAGAGATTGAGCATTAATCAAACTGGAAAAAGTCCACATCTCT 253

Qy 61 GluLeuLeuPheAspTPGlyThrThrAsnCysThrValGlyAaspLeuValAaspLeu 80
Db 254 GAATTACTGTTGACTGGGACCAACAATTGCACAGTTGATGATCTTTTG 313

Qy 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAaspAlaValPro 98
Db 314 ATCCAAATGAATTTTTCCTCTGCGAGTCTTTTGTCCCGATGCTGTTCCC 367

RESULT 9
AX431318 2817 bp DNA linear PAT 28-JUN-2002
LOCUS Sequence 27 from Patent WO0240680.
DEFINITION AX431318
ACCESSION AX431318
VERSION AX431318.1 GI:21656187
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Pawlowski, K., Fiorentino, L., Godzik, A., Lee, S.H., Reed, J.C.,
Roth, W. and Steiner-Weber, F.
Novel death domain proteins
Patent: WO 0240680-A 27 23-MAY-2002;
JOURNAL BURNHAM INST (US)

FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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/note="unnamed protein product"
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/db_xref="GI:21656188"

CDS
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SDTRFHSFSEYELKVNNTNFERPI SVGKMGEGGQVYKGVNNTTAAVKKLAAM
VDITTEELKQFDOETKVMKCOHNLVELLGFSSPDGDLCLVYVYVNGSLDLRLSC
LDGTPPLPSWNRCKIAGANGINFLIENHHRDIKSNIIILDEAPTAISDPLGRL
ASERFQTVNTRIVGTATYMAPEALRGEITTPSDYSFVVLLEITITGIPAYDENEH
POLLLDIKEIEDEKTEIDYIDIKKNADUSTVEAMYSGASQCRHEKKKNSPDIKKY
HOLLQEWNTAS"

ORIGIN

Alignment Scores:
Pred. No.: 2,17e-60 Length: 2817
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

Qy 1 ThrTyrValArgCysLeuAenValGlyLeuIleArgLysLeuSerAaspPheIleaspPro 20
Db 74 ACATATGCGCTGCCCTCAATGTGGACTAATVAGAAAGCTGCAGATTATTAATGATCCT 133

Qy 21 GlnGluGlyTTPylsYlsLeuAlaValAlaIleYlsYsProSergLYAaspAargTYr 40
Db 134 CAAGAAGATGGAAGAGATTAGCTGTAGCTATTAATAAACATCTGCGATGATAGATAC 193

Qy 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
Db 194 AATCAGTTTCACATAGAGAGATTGAGCATTAATCAAACTGGAAAAAGTCCACATCTCT 253

Qy 61 GluLeuLeuPheAspTPGlyThrThrAsnCysThrValGlyAaspLeuValAaspLeu 80
Db 254 GAATTACTGTTGACTGGGACCAACAATTGCACAGTTGATGATCTTTTG 313

Qy 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAaspAlaValPro 98
Db 314 ATCCAAATGAATTTTTCCTCTGCGAGTCTTTTGTCCCGATGCTGTTCCC 367

RESULT 9
AX431318 2817 bp DNA linear PAT 28-JUN-2002
LOCUS Sequence 27 from Patent WO0240680.
DEFINITION AX431318
ACCESSION AX431318
VERSION AX431318.1 GI:21656187
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Pawlowski, K., Fiorentino, L., Godzik, A., Lee, S.H., Reed, J.C.,
Roth, W. and Steiner-Weber, F.
Novel death domain proteins
Patent: WO 0240680-A 27 23-MAY-2002;
JOURNAL BURNHAM INST (US)

FEATURES
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/db_xref="taxon:9606"
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/protein_id="CAD37285.1"
/db_xref="GI:21656188"

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DVRYNQFHIRFALLQTKSPFSELLFDWGTNCTVGDVLVLQNEFPAPSLILP
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SDTRFHSFSEYELKVNNTNFERPI SVGKMGEGGQVYKGVNNTTAAVKKLAAM
VDITTEELKQFDOETKVMKCOHNLVELLGFSSPDGDLCLVYVYVNGSLDLRLSC
LDGTPPLPSWNRCKIAGANGINFLIENHHRDIKSNIIILDEAPTAISDPLGRL
ASERFQTVNTRIVGTATYMAPEALRGEITTPSDYSFVVLLEITITGIPAYDENEH
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HOLLQEWNTAS"

ORIGIN

Alignment Scores:
Pred. No.: 2,17e-60 Length: 2817
Score: 517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-001-254-6 (1-98) x AK431318 (1-2817)

QY 1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgIysLeuSerAspPheIleAspPro 20
 DB 74 ACATATGTCGGCTGCTCAATGTTGACTATATGAGAGCTGTGAGATTTTATGATCCT 133

QY 21 GlnGluGlyTyrPheIysLeuAlaValAlaIleIysIysProSerGlyAspAspArgTyr 40
 DB 134 CAAGAAGATGAGAGAGATTGAGCTGATTAATAAACCATTCTGTGATGATGATAC 193

QY 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyIysSerProThrSer 60
 DB 194 AATCAGTTTCACATAGAGAGATTGAGACATTAATCTCAAACTGAAAAAGTCCCATCTTCT 253

QY 61 GluLeuLeuPheAspTyrGlyTyrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
 DB 254 GAATTAAGTCTTTGACTGCGGACCAAAATTCGACAGTTGTGTGATCTTTG 313

QY 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuProAspAlaValPro 98
 DB 314 ATCCAAATGAAATTTTGTCTCTCGAGCTTTTGTCTCCAGATGCTGTTCCC 367

RESULT 10
 AF155118 2817 bp mRNA linear PRI 05-JAN-2000
 LOCUS Homo sapiens putative protein kinase NY-REN-64 antigen mRNA,
 DEFINITION complete cds.
 ACCESSION AF155118
 VERSION AF155118.1 GI:5360130
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 2817)
 Scanlan,M.J., Jordan,J.D., Williamson,B., Stockert,E., Bander,N.H.,
 Jongeneel,V., Gure,A.O., Jager,D., Jager,E., Knuth,A., Chen,Y.-T.
 and Old,L.J.
 Antigens recognized by autologous antibody in patients with
 renal-cell carcinoma
 Int. J. Cancer 83 (4), 456-464 (1999)
 99438124
 10508479
 2 (bases 1 to 2817)
 Scanlan,M.J., Jordan,J.D., Williamson,B., Stockert,E., Bander,N.H.,
 Jongeneel,V., Gure,A.O., Jager,D., Jager,E., Knuth,A., Chen,Y.-T.
 and Old,L.J.
 Direct Submission
 Submitted (28-MAY-1999) Ludwig Institute, Sloan-Kettering
 Institute, 1275 York Ave, New York, NY 10021, USA
 Location/Qualifiers
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 /cell_line="1973/10-4"
 /cell_type="renal cell carcinoma"
 50..1432
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 SDTPHSPFYEIKNTNNPDERPISUGANGSGEGRGVYKGYANTTVAVKLAAM
 VDTTTERIKQOPDDEIKYMAKQGNINVELGFSDDGDLCLVYVMPNGSLDELSC
 LDGTPPUSMHRCKTLAGGANGINFLHNHHIHRDKANILILDEAPFAKISDFGLAR
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 HOLIQEMTAS"

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
2,17e-60	517.00	100.00%	100.00%	100.00%	9	2817	98	0	0	0	0

US-10-001-254-6 (1-98) x AF155118 (1-2817)

QY 1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgIysLeuSerAspPheIleAspPro 20
 DB 74 ACATATGTCGGCTGCTCAATGTTGACTATATGAGAGCTGTGAGATTTTATGATCCT 133

QY 21 GlnGluGlyTyrPheIysLeuAlaValAlaIleIysIysProSerGlyAspAspArgTyr 40
 DB 134 CAAGAAGATGAGAGAGATTGAGCTGATTAATAAACCATTCTGTGATGATGATAC 193

QY 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyIysSerProThrSer 60
 DB 194 AATCAGTTTCACATAGAGAGATTGAGACATTAATCTCAAACTGAAAAAGTCCCATCTTCT 253

QY 61 GluLeuLeuPheAspTyrGlyTyrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
 DB 254 GAATTAAGTCTTTGACTGCGGACCAAAATTCGACAGTTGTGTGATCTTTG 313

QY 81 IleGlnAsnGluPhePheAlaProAlaSerLeuLeuProAspAlaValPro 98
 DB 314 ATCCAAATGAAATTTTGTCTCTCGAGCTTTTGTCTCCAGATGCTGTTCCC 367

RESULT 11
 AK000528 2820 bp mRNA linear PRI 13-SEP-2003
 LOCUS Homo sapiens cDNA FLJ20521 fls, clone KAT10395.
 DEFINITION AK000528
 ACCESSION AK000528
 VERSION AK000528.1 GI:7020683
 KEYWORDS oligo capping; fls (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1
 Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Teshiro,H.,
 Ota,T., Suzuki,Y., Ohyashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
 Nakamura,T., Isogai,T. and Sugano,S.
 NEDO human cDNA sequencing project
 Unpublished
 2 (bases 1 to 2820)
 Sugano,S., Suzuki,Y., Ota,T., Ohyashi,M., Nishi,T., Isogai,T.,
 Shibahara,T., Tanaka,T. and Nakamura,Y.
 Direct Submission
 Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science,
 University of Tokyo, Department of Virology, Shirokane-dai, 4-6-1,
 Minato-ku, Tokyo 108-8639, Japan (E-mail:flcdna@ms.u-tokyo.ac.jp,
 Tel:81-3-5449-5286, Fax:81-3-5449-5416)
 NEDO human cDNA sequencing project supported by Ministry of
 International Trade and Industry of Japan; cDNA full insert
 sequencing; Research Association for Biotechnology; cDNA library
 construction; 5'- & 3'-end one pass sequencing; Department of
 Virology and Human Genome Center, Institute of Medical Science,
 University of Tokyo (partly supported by Science and Technology
 Agency).
 Location/Qualifiers
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FEATURES

source

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ORIGIN

Alignment Scores:

Score: 2,176-60 Length: 2820
517.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-001-254-6 (1-98) x AK000528 (1-2820)

QY 1 ThrTyrValArgCysLeuAenValGlyLeuILEarGlyLeuSerAspPheILEaspPro 20
Db 54 ACATATGCGCGCTCCCTCAATGTTGACTAATTAAGAACTGTGACAGATTATTATGATCCT 113
QY 21 GlnGlnGlyTTPlybysyLeuAlaValAlaIlelysybProserGlyAspAspArgTyr 40
Db 114 CAAGAAGATGAAAGAACTGACCTGATTAATAAAACATCTGCGATGATGATAC 173
QY 41 AsnGlnPheHisILEarGArgPheGluAlaLeuLeuGlnThrGlyLySerProThrSer 60
Db 174 AATCAGTTTCACATRAGAGATTGAAACATTACTTCAAACTGAAAAAGTCCCACTTCT 233
QY 61 GluLeuLeuPheAspTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80
Db 234 GAATTACTGTTTGACTGGGCGACCAAAATGACACAGTGTGATCTTGTGATCTTTTG 293
QY 81 IleGlnGlnGlyPhePheAlaProAlaSerLeuLeuProAspAlaValPro 98
Db 294 ATCCAAATGAATTTTGTCTCGCGAGTCTTTTGTCTCCAGATGCTTCCC 347

RESULT 12

LOCUS AY283671 1381 bp mRNA linear PRI 17-JUN-2003
DEFINITION Homo sapiens interleukin-1 receptor associated kinase 4 mutant form
ACCESSION AY283671
VERSION AY283671.1 GI:31871819

KEYWORDS

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Medvedev A.E., Lentschat A., Kuhns D.B., Bianco J.C.G.,
Gallin J.I. and Vogel S.N.
Distinct mutations in IRAK-4 confer Hyporesponsiveness to
Lipopolysaccharide and Interleukin-1 in a Patient with Recurrent
Bacterial Infections

J. Exp. Med. (2003) In press
2 (bases 1 to 1381)

Medvedev A.E., Lentschat A., Kuhns D.B., Bianco J.C.G.,
Gallin J.I. and Vogel S.N.
Direct Submission

Submitted (25-APR-2003) Microbiology and Immunology, University of
Maryland, Baltimore, 655 West Baltimore Street, Baltimore, MD
21201-1559, USA

FEATURES

Source

Location/Qualifiers
1..1381
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/gene="IRAK4"
1..657
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CDS

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SDTRFHSFSEFLKNVTNNFDERPISVGNKMGEGGFVYKGYVNNVTAVKLALM
VDITTEELKQFPDEIRKMAKCOHENIVELFSGSDGDLCLVYVMPNGSLDLASC
LDGTPPLSMWRCKIAQAGANGINFLNHHIHDIKSANILLDEAFKASDLGLAR
ASEKFAQVTMTSRIVGTAVAPALRGEITPKSDIYSGVLLLEITGLPQVNEHE
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variation

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/note="site of deletion mutation 2; as compared to GenBank
Accession Number AY283670 and wild-type IRAK4"
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ORIGIN

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Score: 3,246-60 Length: 1381
513.00 Matches: 97
Percent Similarity: 98.98% Conservative: 0
Best Local Similarity: 99.98% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 9 Gaps: 0

US-10-001-254-6 (1-98) x AY283671 (1-1381)

QY 1 ThrTyrValArgCysLeuAenValGlyLeuILEarGlyLeuSerAspPheILEaspPro 20
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QY 21 GlnGlnGlyTTPlybysyLeuAlaValAlaIlelysybProserGlyAspAspArgTyr 40
Db 85 CAAGAAGATGAAAGAACTGACCTGATTAATAAAACATCTGCGATGATGATAC 144
QY 41 AsnGlnPheHisILEarGArgPheGluAlaLeuLeuGlnThrGlyLySerProThrSer 60
Db 145 AATCAGTTTCACATRAGAGATTGAAACATTACTTCAAACTGAAAAAGTCCCACTTCT 204
QY 61 GluLeuLeuPheAspTTPGlyThrThrAsnCysThrValGlyAspLeuValAspLeu 80
Db 205 GAATTACTGTTTGACTGGGCGACCAAAATGACACAGTGTGATCTTGTGATCTTTTG 264
QY 81 IleGlnGlnGlyPhePheAlaProAlaSerLeuLeuProAspAlaValPro 98
Db 265 ATCCAAATGAATTTTGTCTCGCGAGTCTTTTGTCTCCAGATGCTTCCC 318

RESULT 13

LOCUS AX196260 1383 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 2 from Patent WO0151641.
ACCESSION AX196260
VERSION AX196260.1 GI:15386462

KEYWORDS

Homo sapiens (human)
Homo sapiens

REFERENCE

1 Weesche H. and Li S.
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Irak-4: compositions and methods of use

JOURNAL Patent: WO 0151641-A 2 19-JUL-2001;
Tularik Inc. (US)
Location/Qualifiers
FEATURES
source

1. .1383
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SDTRFHSFSELYELKNTNNPDERPISVGKMGEGGVVYKGVVNNNTVAVKKLAM
VITTEELKQDFQEIKVAKCQHENLVELGFSDDDLCLVYVYMPGSLDRISC
LDGTPPLSWHMRCKIAQGANGLFHNHHRDIKSANILLDEAFKISDFGLAR
ASEKPAQVTMTSRIVGTAYMAPALRGETTPKSDIYSFVALLIITGLPAVDEHRE
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ORIGIN

Alignment Scores:
Pred. No.: 3,246-60 Length: 1383
Score: 513.00 Matches: 97
Percent Similarity: 98.98% Conservative: 0
Best Local Similarity: 98.98% Mismatches: 1
Query Match: 99.23% Indels: 0
Gaps: 0

US-10-001-254-6 (1-98) x AX196260 (1-1383)

QY 1 ThrTYrValArgCySeuAenValGlyLeuIlleArgIysSeuSerAappheilleaapPro 20
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QY 21 GINGUGLYTTPLYSLYSLAVALAIALELYSLYSPROSERGIYASPAAPATGYR 40
DB 85 CAAAGAGATGAGAGAGATTAGCTGTAGCTATTAATAAACCACTGTGATGATGATAC 144
QY 41 AengInpHeHsIleArgARpHeGluAlaLeuLeuInHrGlyIysSerProThrsr 60
DB 145 AATCGATTTCACATAGAGATTGAGCATTAATCAACCTGGAAGAAAGTCCACTCTCT 204
QY 61 GluLeuLeuPheAspTPGlyThrThraSncYsThrValGlyAspLeuValAspLeu 80
DB 205 GAATTACGTGTTGATCGGGGACACCAAAATTGACACGCTGGATCTTGGATCTTTTG 264
QY 81 IllegInaEngIupheHeAlaProAlaSerLeuLeuProAspAlaValPro 98
DB 265 ATCCAAATGAATTTTCTCTCGGAGCTCTTTCTCCAGATCTCTTCCC 318

RESULT 14
LOCUS AF445802 1383 bp mRNA linear PRI 20-APR-2002
DEFINITION Homo sapiens interleukin-1 receptor associated kinase 4 (IRAK4)
ACCESSION AF445802
VERSION AF445802.1 GI:20219009
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1383)
AUTHORS Li S., Streiow, A., Fontana, E.J. and Wesche, H.
TITLE IRAK-4: a novel member of the IRAK family with the properties of an
IRAK-kinase
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (8), 5567-5572 (2002)
MEDLINE 21957277

PUBMED 11960013
REFERENCE 2 (bases 1 to 1383)
AUTHORS Suzuki, N., Suzuki, S., Duncan, G.S., Miller, D.G., Wada, T.,
Mitsos, C., Takada, H., Wakeham, A., Irie, A., Li, S., Penninger, J.M.,
Wesche, H., Ohashi, P.S., Mak, T.W. and Yeh, W.C.
TITLE Severe impairment of interleukin-1 and Toll-like receptor
signaling in mice lacking IRAK-4
JOURNAL Nature 416 (6882), 750-756 (2002)
MEDLINE 21959395

PUBMED 11923872
REFERENCE 3 (bases 1 to 1383)
AUTHORS Li, S., Streiow, A., Fontana, E.J. and Wesche, H.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-2001) Biologry I, Tularik Inc., 2 Corporate Drive,
South San Francisco, CA 94080, USA

FEATURES

source

gene
CDS

1. .1383
/organism="Homo sapiens"
/mol_type="mRNA"
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1. .1383
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ORIGIN

Alignment Scores:
Pred. No.: 3,246-60 Length: 1383
Score: 513.00 Matches: 97
Percent Similarity: 98.98% Conservative: 0
Best Local Similarity: 98.98% Mismatches: 1
Query Match: 99.23% Indels: 0
Gaps: 0

US-10-001-254-6 (1-98) x AF445802 (1-1383)

QY 1 ThrTYrValArgCySeuAenValGlyLeuIlleArgIysSeuSerAappheilleaapPro 20
DB 25 ACAATATGCGCGCTGCTCAATGTTGAGCATATAGAGAGCTGCAATTTTATGATCTT 84
QY 21 GINGUGLYTTPLYSLYSLAVALAIALELYSLYSPROSERGIYASPAAPATGYR 40
DB 85 CAAAGAGATGAGAGAGATTAGCTGTAGCTATTAATAAACCACTGTGATGATGATAC 144
QY 41 AengInpHeHsIleArgARpHeGluAlaLeuLeuInHrGlyIysSerProThrsr 60
DB 145 AATCGATTTCACATAGAGATTGAGCATTAATCAACCTGGAAGAAAGTCCACTCTCT 204
QY 61 GluLeuLeuPheAspTPGlyThrThraSncYsThrValGlyAspLeuValAspLeu 80
DB 205 GAATTACGTGTTGATCGGGGACACCAAAATTGACACGCTGGATCTTGGATCTTTTG 264
QY 81 IllegInaEngIupheHeAlaProAlaSerLeuLeuProAspAlaValPro 98
DB 265 ATCCAAATGAATTTTCTCTCGGAGCTCTTTCTCCAGATCTCTTCCC 318

RESULT 15
LOCUS AY283670 1383 bp mRNA linear PRI 17-JUN-2003

DEFINITION Homo sapiens interleukin-1 receptor associated kinase 4 mutant form
ACCESSION 1 (IRAK4) mRNA, complete cds.
VERSION AY283670
KEYWORDS AY283670.1 GI:31871817
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bkaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1383)
AUTHORS Medvedev,A.E., Lentschat,A., Kuhns,D.B., Bianco,J.C.G., Salkowski,C., Zhang,S., Arditi,M., Gallin,J.I. and Vogel,S.N.
TITLE Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to Lipopolysaccharide and Interleukin-1 in a Patient with Recurrent Bacterial Infections
JOURNAL J. Exp. Med. (2003) In press
REFERENCE 2 (bases 1 to 1383)
AUTHORS Medvedev,A.E., Lentschat,A., Kuhns,D.B., Bianco,J.C.G., Salkowski,C., Zhang,S., Arditi,M., Gallin,J.I. and Vogel,S.N.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2003) Microbiology and Immunology, University of Maryland, Baltimore, 655 West Baltimore Street, Baltimore, MD 21201-1559, USA
FEATURES
source location/Qualifiers
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877
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ORIGIN
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Score: 513.00 Matches: 97
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Best Local Similarity: 98.98% Mismatches: 1
Query Match: 99.23% Indels: 0
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US-10-001-254-6 (1-98) x AY283670 (1-1383)
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Db 25 ACATATGTGGCGCTGCTCAATGTGACTAATGTAGAGAGCTGTGATTTATGATCTT 84
Qy 21 GlnGlnGlyTyrPheValValAlaIleLeuValProSerGlyAspAspArgTyr 40

Db 85 CAGCAGAGATGGAAGAGTTAGCTGTAGCTATTAACCAATCTGATGATAGTAC 144
Qy 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLeuSerProThrSer 60
Db 145 AATCAGTTTCACATTAAGAGATTTGAAGCACTTCAAACTGGAAAAAGTCCCATCTTCT 204
Qy 61 GlnLeuLeuPheAspTyrGlyThrThrAsnGlyThrValGlyAspLeuValAspLeuLeu 80
Db 205 GAATTTACTGTTTGACTGGGACACCAAAATGGACAGCTGTATCTTGTGGATCTTTTG 264
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Job time : 3307 secs

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